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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 04:44:13 ; Search time 2105.28 Seconds

(without alignments)
22709.011 Million cell updates/sec

Title: US-09-677-752-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2818	97.2	14177	1	AE001360
3	2777.8	95.9	2934	6	AX155940
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ALIGNMENTS

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LOCUS AX155928 2895 bp DNA
DEFINITION Sequence 171 from Patent WO0140474.
ACCESSION AX155928
VERSION AX155928.1 GI:14537033
KEYWORDS
SOURCE
ORGANISM
Chlamydia sp.
Chlamydia sp.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE
1 (bases 1 to 2895)
Probst,P., Bhalla,A., Skeiky,Y.A., Flinn,S.P. and Scholler,J.
AUTHORS
Compounds and methods for treatment and diagnosis of chlamydial
TITLE
infection
JOURNAL
Patent: WO 0140474-A 171 07-JUN-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
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PAT 22-JUN-2001

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LOCUS AX155940 Sequence 183 from Patent WO0140474
DEFINITION AX155940
ACCESSION AX155940
VERSION AX155940.1 GI:14537039
KEYWORDS

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 DEFINITION Chlamydia muridarum, section 25 of 85 of the complete genome.
 ACCESSION AE002293 AE002160

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VERSION AE002293.1 GI:7190298
KEYWORDS Chlamydia muridarum.
SOURCE Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
ORGANISM Chlamydia muridarum.
REFERENCE 1 (bases 1 to 14482)
AUTHORS Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T.,
Berry, K., Bass, S., Linher, K., Weidman, J., Kouri, H., Craven, B.,
Bowman, C., Dodson, R., Gwin, M., Nelson, W., DeBoy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J., and Fraser, C.M.
Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pneumoniae Ar39
JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)
MEDLINE 20150255
PUBMED 10684935
REFERENCE 2 (bases 1 to 14482)
AUTHORS Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T.,
Berry, K., Bass, S., Linher, K., Weidman, J., Kouri, H., Craven, B.,
Bowman, C., Dodson, R., Gwin, M., Nelson, W., DeBoy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J., and Fraser, C.M.
Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
LOCATION/Qualifiers
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Qy	1970	aacacagaagtcceccataagcgaataactatg-----gggaatatgctgcttggaa	2023
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Qy	2024	cagaaagcttaaaaaatagtgagaaagacttgacacttgatgatacctctcttgggaata	2083
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Query Match      4.7%: Score 136.4; DB 1: Length 300650;
Best Local Similarity 45.9%; Pred. No. 3.1e-21;
Matches 762; Conservative 0; Mismatches 856; Indels 42; Gaps 7;

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OY	2283	aggagaatctctcttccattgtaagaagaagttctcttgctgcagtaaatagttatggcctta	2342
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OY	2643	tcaagccttgagatgtgaaatctggcatacaacacccgttctgtataagacaagaacgaagat	2702
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OY	2703	cgagaccagctccctagccagtaaggatattggtttggtatgtagaagccctcatgcg	2762
Db	7388	GTTTCACACACTACTCTACTCATAGCAATGGAATATGGACACACAGCAAGCACTCCCGTCTCTA	7329
OY	2763	tcatgcaatgtccctataaacttcacaagcaaacacacacttggatgtgtaactctca	2822
Db	7328	TAAATCCGTAGCTGCAGAAAATATAAAAATACTTCCCACTTTTCTCAAGAGTACCTTATC	7269
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Db	7208	TCATTCGACATTTTA 7194	

RESULT	9				
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DEFINITION	Chlamydia muridarum, section 25 of 85 of the complete genome.				
ACCESSION	AE002293	AE002160			
VERSION	AE002293.1	GI:7190298			
KEYWORDS					
SOURCE	Chlamydia muridarum.				
ORGANISM	Chlamydia muridarum				
REFERENCE	Bacteria: Chlamydiales: Chlamydiaceae: Chlamydia.				
AUTHORS	1 (bases 1 to 14482)				
	Read, T.D., Bricham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,				
	White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Ulteback, T.,				
	Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,				
	Bowman, C., Dodson, R., Gwinn, M., Nelson, W., Deboy, R., Kolonay, J.,				
	McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.				

McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.

[illegible]

Query Match	2.0%;	Score 56.6;	DB 1;	Length 14482;
Best Local Similarity	55.8%;	Pred. No. 0.011;		
Matches 129;	Conservative 0;	Mismatches 99;	Indels 3;	Gaps 1;

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LOCUS	2343 bp	DNM	FBI	22-JUN-2001
DEFINITION	Sequence 170 from Patent WO0140474.			
ACCESSION	AX155927			

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VERSION . AX155927.1  GI:14537032
KEYWORDS

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ORGANISM Chlamydia sp.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE	AUTHORS	TITLE
1 (pages 1 to 2949)	Probst, P., Bhattacharya, A., Skeelky, Y. A., Fling, S. P. and Scholler, J.	Compounds and methods for treatment and diagnosis of chlamydia

infection
Patent: WO 0140474-A 170 07-JUN-2001;
JOURNAL

FEATURES	Location/Qualifiers
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/organism="Chlamydia sp."
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Bacteria;	Chlamydiales; Chlamydiaceae; Chlamydia.

AUTHORS Probst, P., Bhatia, A., Skeiky, Y. A., Fling, S. P. and Scholler, J.
TITLE Compounds and methods for treatment and diagnosis of chlamydial infection
REFERENCE *Journal of Clinical Investigation* 103: 1823-1832 (2000)
COMMENT 0140474-3 1823-02 JUN-2001

CORIXA CORPORATION (US)
Location/qualifiers

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[illegible]

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DEFINITION	LOCUS	AE003782	298283 bp	DNA	INV	04-OCT-2000
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Section 2						

of 3, complete sequence.
ACCESSION AE003782 AE002725

VERSION	2003/02/2	01.10.2003
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ORGANISM *Drosophila melanogaster*

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MEDLINE 99206606
 PUBMED 10192388
 REFERENCE 3 (bases 1 to 14177)
 AUTHORS Stephens,R.S., Kaiman,S., Lammel,C.J., Fan,J., Marathe,R.,
 Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q.,
 Koonin,E.V. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (20-MAY-1998) Program in Infectious Diseases, University
 of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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2	2821.2	97.3	2895	22	AAH36256	Chlamydia trachoma
3	2819.6	97.3	2895	21	AAA64753	C. trachomatis pmp
4	2777.8	95.9	2934	21	AAA64759	C. trachomatis pmp
5	2777.8	95.9	2934	22	AAH56262	Chlamydia trachoma
6	136.4	4.7	273354	21	AAAC8164	Chlamydia pneumoniae
c	134.8	4.7	1230025	20	AAAX1990	Nucleotide sequen
7	134.6	4.5	3003	21	AAAZ8711	C. pneumoniae CPN1
8	131.6	4.5	3200	21	AAA28710	C. pneumoniae CPN1
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c	118.6	4.1	936	22	AAAF38252	Oligonucleotide D1
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C	15	118.6	4.1	936	22	AAFS8255	Oligonucleotide D1
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C	18	115.8	4.0	936	22	AAFS8257	Oligonucleotide D1
C	19	115.8	4.0	936	22	AAFS8259	Oligonucleotide D2
C	20	115.8	4.0	936	22	AAFS8262	Oligonucleotide D1
C	21	115.8	4.0	936	22	AAFS8255	Oligonucleotide D1
C	22	115.8	4.0	3096	21	AAAS0038	DNA encoding Chlam
C	23	89.6	3.1	2792	21	AAAS2813	C. pneumoniae CPN1
C	24	89.6	3.1	3000	21	AAAS2812	C. pneumoniae CPN1
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C	35	45.2	1.6	1941	22	AAHS58329	DNA encoding Chlam
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C	38	41.6	1.4	3354	20	AAAB60556	Seq ID No.: 23 of W
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C	43	40.8	1.4	900	20	AAAB56160	B. burgdorferi ant
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XX	Vaccine; eye disease; conventional trachoma; nonendemic trachoma;	
KW	paratrachoma; inclusion conjunctivitis; genital disease; peritrichitis;	
KW	nongonococcal urethritis; epididymitis; cervicitis; salpingitis;	
KW	bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.	
XX	Chlamydia trachomatis.	
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PR	28-NOV-1997;	97ER-0015041.
PR	17-DEC-1997;	97ER-0016034.
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DR		
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PT	Genome sequence of Chlamydia trachomatis	


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AC AAA64753;
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DT 02-FEB-2001 (first entry)
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KW Chlamydial infection; sexually transmitted disease;
KW pelvic inflammatory disease; PID; tubal obstruction; infertility;
KW trachoma; blindness; acute respiratory tract infection;
KW atherosclerosis; coronary heart disease; antibacterial; ss.
XX
OS Chlamydia trachomatis.
XX
PN WO200034483-A2.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999; 99WO-US29012.
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PR 08-DEC-1998; 98US-0208277.
PR 08-APR-1999; 99US-0288594.
PR 01-OCT-1999; 99US-0410568.
PR 22-OCT-1999; 99US-0426571.
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DR WPI: 2000-431303/37.
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PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection
XX
PT amino acid sequence encoded by polynucleotide sequence
XX
PS Claim 1: Pages 173-174: 256pp; English.
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```
XX The present invention relates to new nucleic acid sequences and the
CC proteins encoded by the nucleic acid sequences. The encoded proteins
CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
CC proteins are useful for the serodiagnosis and treatment of Chlamydia
CC infection. Chlamydiae are intracellular bacterial pathogens that are
CC responsible for a wide variety of human infections. C. trachomatis
CC infection is one of the most common sexually transmitted diseases and can
CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
CC and infertility. Trachoma due to ocular infection with C. trachomatis is
CC the leading cause of preventable blindness worldwide. C. pneumoniae is a
CC major cause of acute respiratory tract infections in humans and is also
CC thought to play a role in the pathogenesis of atherosclerosis and
CC coronary heart disease. The present sequence is a nucleic acid sequence
CC isolated in the present invention.
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S0 Sequence 2895 BP: 866 A; 633 C; 558 G; 838 T; 0 other.

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Best Local Similarity 98.6%; Pred. No. 0;
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OY 601 ttatgagacaacatctgtattccaactaacacagcagaagaagtgagcgtatctatgct 660
DB 601 ttatgagacaacatctgtattccaactaacacagcagaagaagtgagcgtatctatgct 660
OY 598 ttatgagacaacatctgtattccaactaacacagcagaagaagtgagcgtatctatgct 657
DB 598 ttatgagacaacatctgtattccaactaacacagcagaagaagtgagcgtatctatgct 657
OY 661 ggaagagcattatgacgcgtaaaccttctgtgtgaggaagaatcagctgtttctc 720
DB 661 ggaagagcattatgacgcgtaaaccttctgtgtgaggaagaatcagctgtttctc 720
OY 658 ggaagagcattatgacgcgtaaaccttctgtgtgaggaagaatcagctgtttctc 717
DB 658 ggaagagcattatgacgcgtaaaccttctgtgtgaggaagaatcagctgtttctc 717
OY 721 ttgacagagagagcagatctctcctcatctgttcttcaacaggaatcgtgttaacatc 780
DB 721 ttgacagagagagcagatctctcctcatctgttcttcaacaggaatcgtgttaacatc 780
```

```
RESULT 4
AA64759
ID AAA64759 standard: DNA: 2934 BP.
XX
AC AAA64759:
XX
DT 02-FEB-2001 (first entry)
XX
DE C. trachomatis pmpE gene coding sequence minus the signal sequence.
XX
KM Chlamydial infection; sexually transmitted disease;
KM pelvic inflammatory disease; PID; tubal obstruction; infertility;
KM trachoma; blindness; acute respiratory tract infection;
KM atherosclerosis; coronary heart disease; antibacterial; ss.
XX
OS Chlamydia trachomatis.
XX
PN MO20034483-A2.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999: 99WO-US29012.
XX
PR 08-DEC-1998: 98US-0208277.
PR 08-APR-1999: 99US-0288594.
PR 01-OCT-1999: 99US-0410568.
PR 22-OCT-1999: 99US-0426571.
XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ.
XX
DR WPI: 2000-431303/37.
XX
PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection
PT comprises immunogenic portion of Chlamydia antigen, which comprises
PT amino acid sequence encoded by polynucleotide sequence
XX
XX
XX Claim 1: Pages 200-201. 256pp: English.
XX
XX
CC The present invention relates to new nucleic acid sequences and the
CC proteins encoded by the nucleic acid sequences. The encoded proteins
CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
CC proteins are useful for the serodiagnosis and treatment of Chlamydia
CC infection. Chlamydiae are intracellular bacterial pathogens that are
CC responsible for a wide variety of human infections. C. trachomatis
CC infection is one of the most common sexually transmitted diseases and can
CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
CC and infertility. Trachoma due to ocular infection with C. trachomatis is
CC the leading cause of preventable blindness worldwide. C. pneumonia is a
CC major cause of acute respiratory tract infections in humans and is also
CC thought to play a role in the pathogenesis of atherosclerosis and
CC coronary heart disease. The present sequence is a nucleic acid sequence
CC isolated in the present invention.
XX
XX
SQ Sequence 2934 BP: 875 A: 645 C: 575 G: 839 T: 0 other:
Query Match 95.98; Score 2777.8; DB 21; Length 2934;
Best Local Similarity 98.68; Pred. No. 0;
Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
```

```
Db 205 tgcatactcgataaactcgatcatatctggtatcttacaacaaactcccaatgaagga 264
Oy 226 gctctgtcacatacaacagattaccataagcttttgaatacaacaaagaagattat 285
Db 265 gctctgtcacatacaacagattaccataagcttttgaatacaacaaagaagattat 324
Oy 286 ttgtcaaaaaatctacccctgaagaagtgtgtgcatgtgttatagtcgatcccaatct 345
Db 325 ttgtcaaaaaatctacccctgaagaagtgtgtgcatgtgttatagtcgatcccaatct 384
Oy 346 cctacccgtggaattctgtatatacaataggtccgttaacttttgaataaactgtgtgc 405
Db 385 cctacccgtggaattctgtatatacaataggtccgttaacttttgaataaactgtgtgc 444
Oy 406 agaccattacatcgagaatcccaatcgactttaaataaagaagagcggaacc 465
Db 445 agaccattacatcgagaatcccaatcgactttaaataaagaagagcggaacc 501
Oy 466 attcatgctcaaaatctttacataaataatcataatgaatgtgtcggaattatgaagaa 525
Db 502 attcatgctcaaaatctttacataaataatcataatgaatgtgtcggaattatgaagaa 561
Oy 526 ttctctatgtccgaaggagagccatagtagtaccgttaactccttgtgtgagcgagaat 585
Db 562 ttctctatgtccgaaggagagccatagtagtaccgttaactccttgtgtgagcgagaat 621
Oy 586 cagctctgttttctttatgtgacaacactgtatcaacataaagcagaggaagagt 645
Db 622 cagctctgttttctttatgtgacaacactgtatcaacataaagcagaggaagagt 681
Oy 646 ggcgcatactatgtcgtgaagacagcaatcttltgagagtaataacctgcatctcttct 705
Db 682 ggcgcatactatgtcgtgaagacagcaatcttltgagagtaataacctgcatctcttct 741
Oy 706 atcaataagcctgtgtgtcagagagagagatcttccctatctgttcttaacagga 765
Db 742 atcaataagcctgtgtgtcagagagagagatcttccctatctgttcttaacagga 801
Oy 766 aatcgtgttaacatcgctttctataacacatcgctgtctttaaanaatgtgaagaacagcttct 825
Db 802 aatcgtgttaacatcgctttctataacacatcgctgtctttaaanaatgtgaagaacagcttct 861
Oy 826 tcaagaagcttctgtatgtgagagacaaatlaaagtaactcgcctagatgttacaaggaat 885
Db 862 tcaagaagcttctgtatgtgagagacaaatlaaagtaactcgcctagatgttacaaggaat 921
Oy 886 cgtgtgaagatcctttttagtgaacatatcacaaaaaatatgtgcgagcatttaagct 945
Db 922 cgtgtgaagatcctttttagtgaacatatcacaaaaaatatgtgcgagcatttaagct 981
Oy 946 cctgtgaagatcctttttagtgaacatatcacaaaaaatatgtgcgagcatttaagct 1005
Db 982 cctgtgaagatcctttttagtgaacatatcacaaaaaatatgtgcgagcatttaagct 1041
Oy 1006 aaggggggcgtatctatataatagacaggaacacagcaatcttcgtccgagccgcat 1065
Db 1042 aaggggggcgtatctatataatagacaggaacacagcaatcttcgtccgagccgcat 1101
Oy 1066 gctattattttaaagaataatgtgaactaattgaactaattgaactaattgaactaattga 1125
Db 1102 gctattattttaaagaataatgtgaactaattgaactaattgaactaattgaactaattga 1161
Oy 1126 tcaagtaatcctcctcagaagaataatgaataacagtagcaagcctcctcgtgtgaattcta 1185
Db 1162 tcaagtaatcctcctcagaagaataatgaataacagtagcaagcctcctcgtgtgaattcta 1221
Oy 1186 ttaggaagcaggaagtagcaaaatttaattttagtgcctatgtgaagttagcaatga 1245
Db 1222 ttaggaagcaggaagtagcaaaatttaattttagtgcctatgtgaagttagcaatga 1281
Oy 1246 ggggtcctgtgtcctcaataaaggaagctgatacaaacaggtcgtgtatttttcaaga 1305
Db 1282 ggggtcctgtgtcctcaataaaggaagctgatacaaacaggtcgtgtatttttcaaga 1341
```

XX Claim 1; Page 207; 295pp; English.
 PS The present nucleotide sequence is provided in a specification
 CC relating to compounds and methods for the treatment and diagnosis of
 CC chlamydial infection. The compounds provided include polypeptides and
 CC fusion proteins comprising immunogenic portions of Chlamydia antigens
 CC and DNA sequences encoding such polypeptides. They are useful for
 CC vaccinating against chlamydial infection, which causes pelvic
 CC inflammatory disease, trachoma, acute respiratory tract infections,
 CC atherosclerosis and heart disease.
 CC
 XX
 SO Sequence 2934 BP; 875 A; 645 C; 575 G; 839 T; 0 other:
 Query Match 95.9%; Score 2777.8; DB 22; Length 2934;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
 QY 46 ggactagctagaagaggttccttccttagaatcttcttatgcccgaactcagttccagatcct 105
 DB |||||||
 DB 85 ggactagctagaagaggttccttccttagaatcttcttatgcccgaactcagttccagatcct 144
 QY 106 acgaagaagctgcctacataaataatagtttgacagagagacacccacacatctcactaac 165
 DB |||||||
 DB 145 acgaagaagctgcctacataaataatagtttgacagagagacacccacacatctcactaac 204
 QY 166 tgcatactcgataaactacgcgtacatactggtcattctacaaaaaactcccaatgaagga 225
 DB |||||||
 DB 205 tgcatactcgataaactacgcgtacatactggtcattctacaaaaaactcccaatgaagga 264
 QY 226 gctcgtgcacaataacagattaccttaagctttttgtatcacaaaagaagagttttat 285
 DB |||||||
 DB 265 gctcgtgcacaataacagattaccttaagctttttgtatcacaaaagaagagttttat 324
 QY 286 ttgtcaaaaaaactcacccctgaagaagtgtgtgctgattgtatgcagtcgcccaattct 345
 DB |||||||
 DB 325 ttgtcaaaaaaactcacccctgaagaagtgtgtgctgattgtatgcagtcgcccaattct 384
 QY 346 cctacagctgagagatcgttgatacaataagtcctcgttaactcttggaaaataaactctgttc 405
 DB |||||||
 DB 385 cctacagctgagagatcgttgatacaataagtcctcgttaactcttggaaaataaactctgttc 444
 QY 406 agacatttaactcaggaatccttaactgacgtgttataaataagaagaagcgagagcc 465
 DB |||||||
 DB 445 agacatttaactcaggaatccttaactgacgtgttataaataagaagaagcgagagcc 501
 QY 466 attcatgctcaaaactcttatacataatacaatcatgatagtgtcggattcttagaagaac 525
 DB |||||||
 DB 502 attcatgctcaaaactcttatacataatacaatcatgatagtgtcggattcttagaagaac 561
 QY 526 ttctctatgtccgagagagagccatagtagccgctaataaccttctgttggcgagaat 585
 DB |||||||
 DB 552 ttctctatgtccgagagagagccatagtagccgctaataaccttctgttggcgagaat 621
 QY 566 cagttctgttttcttcttatgagacaacatctgtatccaacaaataacgcaagaagaagt 645
 DB |||||||
 DB 622 cagttctgttttcttcttatgagacaacatctgtatccaacaaataacgcaagaagaagt 681
 QY 646 ggcgctatactatgcggaacgagcaatcttcttgagagtaaatcgtcattcttcttc 705
 DB |||||||
 DB 682 ggcgctatactatgcggaacgagcaatcttcttgagagtaaatcgtcattcttcttc 741
 QY 706 atcaataacgacctgttgcagagagagcgatctctccctcatctgttcttaacagga 765
 DB |||||||
 DB 742 atcaataacgacctgttgcagagagagcgatctctccctcatctgttcttaacagga 801
 QY 766 aatcgttgtaaatcgtttcttatacaaatcgtctttaaataatgtaaaaacagcttct 825
 DB |||||||
 DB 802 aatcgttgtaaatcgtttcttatacaaatcgtctttaaataatgtaaaaacagcttct 861
 QY 826 tcagaagcttctgatacgaggaacatlaaagtaactcgcctgatatcttaacagcaat 885
 DB |||||||

DB 862 tcagaagcttctgatacgagagcaatlaaagtaactcgcctgatatgttaccagcaat 921
 QY 886 cctgttagagatcttttttagtgacatatcacaaaaaataatgctggagctattacgt 945
 DB |||||||
 DB 922 cctgttagagatcttttttagtgacatatcacaaaaaataatgctggagctattacgt 981
 QY 946 cctgttagtacccttagtgataatgcccctactactcttataaacaataatgcacaat 1005
 DB |||||||
 DB 982 cctgttagtacccttagtgataatgcccctactactcttataaacaataatgcacaat 1041
 QY 1006 aaggggggcgtatctatatatagaggaacacagcaactccaataattctgcgcagcccat 1065
 DB |||||||
 DB 1042 aaggggggcgtatctatatatagaggaacacagcaactccaataattctgcgcagcccat 1101
 QY 1066 gctattatttttaagaaataattgtgactaatgttaactaatgcaaatgtaccagtag 1125
 DB |||||||
 DB 1102 gctattatttttaagaaataattgtgactaatgttaactaatgcaaatgtaccagtag 1161
 QY 1126 tcagctaatcctccttagaagaataatgcataacagtagcaagctcctctgttgaattcta 1185
 DB |||||||
 DB 1162 tcagctaatcctccttagaagaataatgcataacagtagcaagctcctctgttgaattcta 1221
 QY 1186 ttagaagcaggagtagcacaataatttaattttatgatcctattggaattagcaatgca 1245
 DB |||||||
 DB 1222 ttagaagcaggagtagcacaataatttaattttatgatcctattggaattagcaatgca 1281
 QY 1246 ggggtctcgtgtccttctaataagaagaagtgtgaacaggctcgtgttatcttcagga 1305
 DB |||||||
 DB 1282 ggggtctcgtgtccttctaataagaagaagtgtgaacaggctcgtgttatcttcagga 1341
 QY 1306 gctactgttaattctgcgaattcttcaacaagcaatttcaacaacaaacacctgcacc 1365
 DB |||||||
 DB 1342 gctactgttaattctgcgaattcttcaacaagcaatttcaacaacaaacacctgcacc 1401
 QY 1366 cttaactctcgaatagtttcttctatgtagagaatcatalgctcagcttaacgtatcgca 1425
 DB |||||||
 DB 1402 cttaactctcgaatagtttcttctatgtagagaatcatalgctcagcttaacgtatcgca 1461
 QY 1426 ttcaacaaacagtgagggtgtgttctctcttggaatgagcaggtctcgtgttcataaa 1485
 DB |||||||
 DB 1462 ttcaacaaacagtgagggtgtgttctctcttggaatgagcaggtctcgtgttcataaa 1521
 QY 1486 aatgtgcaggaattctcgtcagcaatgcctcctataacacctaagaacatctgattgaat 1545
 DB |||||||
 DB 1522 aatgtgcaggaattctcgtcagcaatgcctcctataacacctaagaacatctgattgaat 1581
 QY 1546 ctctcttcacatctgaaagaagtgtgctgagatctccttattgttgggtagagcctacaat 1605
 DB |||||||
 DB 1582 ctctcttcacatctgaaagaagtgtgctgagatctccttattgttgggtagagcctacaat 1641
 QY 1606 aacagcaataactatacagcagatatcgtcagctactcctttcatttaagtatgtaaaac 1665
 DB |||||||
 DB 1642 aacagcaataactatacagcagatatcgtcagctactcctttcatttaagtatgtaaaac 1701
 QY 1666 tcaactatgtagctatgaggaattcctcttataatcacagatctaaacgcatgctgtg 1725
 DB |||||||
 DB 1702 tcaactatgtagctatgaggaattcctcttataatcacagatctaaacgcatgctgtg 1761
 QY 1726 tcatcacagcctatgctatctatcttcgaagctatgataaacgctaagatctgattg 1785
 DB |||||||
 DB 1762 tcatcacagcctatgctatctatcttcgaagctatgataaacgctaagatctgattg 1821
 QY 1786 atggaatttttgggactaaatgctcctcatctatgtagtgcgaagactttggagcttggggc 1845
 DB |||||||
 DB 1822 atggaatttttgggactaaatgctcctcatctatgtagtgcgaagactttggagcttggggc 1881
 QY 1846 tgggcacaaactcaagatccagaaacagcatctcagcaacatcacagatccacaaaaa 1905
 DB |||||||
 DB 1882 tgggcacaaactcaagatccagaaacagcatctcagcaacatcacagatccacaaaaa 1941
 QY 1906 gccaatagattccatagaaacttatctagcttggctctcgtctggtatgtctccctagc 1965
 DB |||||||
 DB 1942 gccaatagattccatagaaacttatctagcttggctctcgtctggtatgtctccctagc 2001

Db	2532	ttgnaacatcccaacgatttagcgatggtatggtatgggacatcac---ctccagctctaca	2588
Qy	2378	cccaaggaagaataatctaacatctccaagggagcttccgtagtctaaacgattggagtgctg	2437
Db	2589	tccgtccacatcaagaagaacgagcgaaggaacgtgtatagccatcatcaatacaacagcta	2648
Qy	2438	tttttttgctcccccataagaaacccctttggatccaagcatatgacagctcccttt	2497
Db	2649	tcggcgtctcttccctcttggaac-----agaatccatcttaccctcagccgctgcg	2702
Qy	2498	taggtgctcttgatattatctttagcctgtcttcacttttacttgaggtggagcctatccgc	2557
Db	2703	ttcagcaatttgcaatgactgtcttcaccaacaacagcgttcgaagaagttggtgaatcccc	2762
Qy	2558	gaagctttctcacaagaactcctttgatcaatgctcctagcttcctcttggagttaaagta	2617
Db	2763	gaagatttgctctccaagaagcctttctataatctgaacttaccttlaagaaaccaaggaa	2822
Qy	2618	gcttatgaatgcttaccacaagaacccccaagccttggaacttgaatctggcatccaacccg	2677
Db	2823	aatggcagctcaaaattccacgactcccaagaatggagctctagaaccttcttaccacaacgg	2882
Qy	2678	tctcgtatagaacaagaacacggagatcgcgaccagctctccttaccgtaaggtattgt	2737
Db	2883	tactctatcaacaataatcccccaatctggttcacgctacttgcgagcgaggtccctggg	2942
Qy	2738	tctgtagtggaagccctcatcgcgctcatgcatgtctctataaaatctcacagaacaac	2797
Db	2943	atacccttaggcataactatgcttcgcgaatgcttlaaggtacaaagctccacaatcaaacgt	3002
Qy	2798	aaccttggaattggttaacctctcatcttccagtatcatgattcctaccccttcaacct	2857
Db	3003	cgcctcttcgctctctctgcactctatctctggatbaccagaagatcgtctccctcgacat	3062
Qy	2858	tctgtaattatccaalggggaatcgctcgcgattica	2897
Db	3063	ctacgcacatctccaagcagcgaagctacttaaatctca	3102
RESULT 10			
ID	AAF58252/C		
XX	AAF58252 standard; DNA; 936 BP.		
AC	AAF58252:		
XX			
DT	24-APR-2001 (first entry)		
XX			
DE	Oligonucleotide D1835.		
XX			
KW	Electron-transfer group; ETM; mismatch; genotyping;		
KW	gene expression; ss.		
XX			
OS	Synthetic.		
XX			
PN	WO200107665-A2.		
XX			
PD	01-FEB-2001.		
XX			
PE	26-JUL-2000; 2000MO-US20476.		
XX			
XX	26-JUL-1999; 990US-0145695.		
PR	17-MAR-2000; 2000US-0190259.		
XX			
PA	(CLIN-) CLINICAL MICRO SENSORS INC.		
XX			
PI	umek RM:		
XX			
DR	WPI: 2001-159728/16.		
XX			
PT	Nucleic acids containing electron-transfer group, useful as labels in		
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses on		
PT	a single surface -		

XX Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
xx

Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match	4.18;	Score 118.6;	DB 22;	Length 936;
Best Local Similarity	1.38;	Pred. No. 2,8e-23;		
Matches	10;	Conservative 480;	Mismatches 299;	Indels 0;
			Gaps	0.

[illegible]

CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.

Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 4.1%; Score 118.6; DB 22; Length 936;
 Best Local Similarity 1.3%; Pred. No. 2.8e-23;
 Matches 10; Conservative 480; Mismatches 299; Indels 0; Gaps 0;

```

Oy 436 gctgttaataaagaagcgagccatcttcctcaaatcttacaataatcat 495
    ||:.....:.....:.....:.....:.....:.....:.....:.....:
Db 789 GCM.....:.....:.....:.....:.....:.....:.....:.....:
Oy 486 aatcatgatggtcggaatttaagaaccttcttctgcccgaaggagccattagt 555
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 729 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 556 accgctaacttctgtgtgagcgagatcagctgttctctcttcttgacaacatc 615
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 669 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 616 tgtattcaactaatacagcaggaaggtgcgctatctatgctggaacgagcaatct 675
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 609 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 676 ttgagagtaataactgcatctctcttcttacaataacgctgtgtgcaaggagcg 735
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 549 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 736 atctctcccatctgttctcttaacagaaatcggtgtaacatgcttctcatacaat 795
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 489 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 796 cgcgtcttaaaaagttagaagaagcttctcaagaagcttcgtaggaggaacataa 855
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 429 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 856 gtaactactgcctagatgttacaagcaatcggtgtaggactctttagtgaacatac 915
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 369 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 916 acaaaaataatggtcgagctattacgctcctgttagtaccctagtgataatgccc 975
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 309 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 976 acctactttataacaacatcgccaataataaggggcgctatctatatacgagaa 1035
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 249 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 1036 agcaactccaattctcgcgacgcgcatattttaaataaataatgtgact 1095
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 189 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 1096 aatgtaactaatgcaaatggtacagtaacgtcaatccctcctgaagaataatgca 1155
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 129 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 1156 acagtgaacagctccctcgtgtaaatctcattagagcagggagtagccaaaattaat 1215
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 69 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 1216 tttaatgat 1224
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 9 W.....:.....:.....:.....:.....:.....:.....:.....:

```

RESULT 13
 AAF58259/C
 ID AAF58259 standard; DNA; 936 BP.
 XX

```

AC AAF58259;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D2004.
XX
KW Election-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM.
XX
DR WPI: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
XX
PS Example 6; Page 128; 1599p; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SO Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 4.1%; Score 118.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 2.8e-23;
Matches 10; Conservative 480; Mismatches 299; Indels 0; Gaps 0;

Oy 436 gctgttaataaagaagcgagccatcttcctcaaatcttacaataatcat 495
    ||:.....:.....:.....:.....:.....:.....:.....:.....:
Db 789 GCM.....:.....:.....:.....:.....:.....:.....:.....:
Oy 496 aatcatgatggtcggaatttaagaaccttcttctgcccgaaggagccattagt 555
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 729 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 556 accgctaacttctgtgtgagcgagatcagctgttctctcttcttgacaacatc 615
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 669 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 616 tgtattcaactaatacagcaggaaggtgcgctatctatgctggaacgagcaatct 675
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 609 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 676 ttgagagtaataacgcgagctctcttcttatacaaaagccctgtgtcgaggaagcg 735
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 549 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 736 atctctcccatctgttctctcaacaggaatcggtgtaacatgcttctcatacaat 795
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 489 W.....:.....:.....:.....:.....:.....:.....:.....:
Oy 796 cgcgtcttaaaaagttagaagaagcttctcaagaagcttcgtaggaggaacataa 855
    :.....:.....:.....:.....:.....:.....:.....:.....:
Db 429 W.....:.....:.....:.....:.....:.....:.....:.....:

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XX Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX Synthetic.
XX WO200107665-A2.
XX 01-FEB-2001.
XX 26-JUL-2000; 2000MO-US20476.
XX 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX Umek RM.
XX WPI; 2001-159728/16.
XX Nucleic acids containing electron-transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface.
XX Example 6; Page 127; 159pp; English.
XX The present invention relates to a composition comprising two nucleic
XX acids each containing an electron-transfer group (ETM) having
XX different redox potentials. The invention is used for electronic
XX detection of nucleic acids, especially of substitutions (mismatches)
XX and single-nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX
SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 4.1%; Score 118.6; DB 22; Length 938;
Best Local Similarity 1.3%; Pred. No. 2,0e-23;
Matches 10; Conservative 460; Mismatches 299; Indels 0; Gaps 0;

QY 436 gctgtaataaataagagagcgagccatcatgctcaaatcttatacaatcat 495
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QY 496 aatcatgatgtgctcgattatgaagaactttctatgtccgagagagccatagt 555
DB 729 AATCATGATGTGCTCGATTATGAAGAACTTCTATGTCGAGAGAGCCATAGT 670
QY 556 accgctaatacttctgttgagcgagaatcagtcctgttctcttataatgacaatc 615
DB 669 ACCGCTAATACTTCTGTGTGAGCGAGAAATCAGTCTCTTCTCTTATAATGACAATC 610
QY 616 tgaatcaactaatacagagagaagagtgcgctatctatgtctggaacgagcaattct 675
DB 609 TGAATCAACTAATAACAGAGAGAAGAGTGCCTATCTATGTCTGGAACGAGCAATTCT 650
QY 676 ttgagagtaataactgcagctcttcttatacaataacgctgtgtgcaagagagcg 735
DB 549 TTGAGAGTAATAACTGCAGCTCTTCTTATACAATAACGCTGTGTGCAAGAGAGCG 730
QY 736 atcttctccctatcgttctcttaacaggaacgctgttaacatcgtttctataacaat 795
DB 489 ATCTTCTCCCTATCGTTCTCTTAACAGGAACGCTGTTAACATCGTTTCTATAACAAT 430
QY 796 cgcgcttaaaaaatgtagaagacgcttctcagaagcttctgtagagagagcaatcaa 855
DB 429 CGCGCTTAAAAAATGTAGAAACGCTTCTCAGAAGCTTCTGTAGAGAGAGCAATCAA 370
QY 856 gtaactactcgcttagatgttacaggaatcgltgtagacatttttagtgacaatc 915
DB 369 GTAACACTCGCTTAGATGTTACAGGAATCGLTGTAGACATTTTGTGACAATC 310

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QY 916 acaaaaaattatgycgagcatattacgctcctgtagtacccttagatgagccct 975
DB 309 ACAAAAAATTATGYCGAGCATATTACGCTCCTGTAGTACCCTTAGATGAGCCCT 250
QY 976 acctactcataacaatatcgccaaataaaggggcgccatcataagagaggaacc 1035
DB 249 ACCTACTCATACAATAATCGCCAAATAAAGGGGCGCCATCATAGAGAGGAACC 190
QY 1036 agcaactccaataattctcgcgacgcgcagcatgtctatttttaatgaataattgtact 1095
DB 189 AGCAACTCCAATAATTCTCGGACGCGCAGCATGTCTATTTTAAATGAATAATTGTACT 130
QY 1096 aatgtaactaatgcaaatgttagaccagtaacgtaacatcctctcagaagaatgcaata 1155
DB 129 AATGTAACTAATGCAAAATGTTAGACCAGTAACGTAACATCCTCTCAGAAGAATGCAATA 70
QY 1156 acagtagcaagcctcctcgtgtgtaaatctatagagcgagagtgccaaaatttaatt 1215
DB 69 ACAGTAGCAAGCCTCCTCGTGTGTAATCTATAGAGCGAGAGTGCCAAAATTTAATT 10
QY 1216 ttatatgat 1224
DB 9 TTTATGAT 1

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Search completed: April 24, 2002, 07:30:35
 Job time: 6187 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 05:09:28 ; Search time 59.26 Seconds
(without alignments)
11075.485 Million cell updates/sec

Title: US-09-677-752-1
Perfect score: 2898
Sequence: 1 aagaaagcgcttcttctt.....aaatgtctgcgattctag 2898

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 351203 segs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	40.6	1.4	1122	2	US-08-915-107-3 Sequence 3, Appli
C 2	40.6	1.4	1122	4	US-09-273-613-3 Sequence 3, Appli
C 3	40.6	1.4	1125	4	US-08-915-107-1 Sequence 1, Appli
C 4	40.6	1.4	1125	4	US-09-273-613-1 Sequence 1, Appli
5	39.2	1.4	1560	1	US-08-356-180-1 Sequence 1, Appli
6	38.4	1.3	807	3	US-08-718-905-1 Sequence 1, Appli
7	38.4	1.3	807	4	US-09-550-497-1 Sequence 1, Appli
8	36.2	1.2	1311	4	US-08-584-760A-66 Sequence 66, Appli
9	35.4	1.2	3513	1	US-07-828-788A-5 Sequence 5, Appli
10	35.4	1.2	3513	1	US-08-278-685-1 Sequence 1, Appli
11	35.4	1.2	3513	1	US-08-278-685-3 Sequence 3, Appli
12	35.4	1.2	3513	1	US-08-277-721-1 Sequence 1, Appli
13	35.4	1.2	3513	1	US-08-277-721-3 Sequence 3, Appli
14	35.4	1.2	3513	1	US-08-602-737-3 Sequence 3, Appli
15	35.4	1.2	3513	4	US-09-001-982-3 Sequence 5, Appli
16	35.4	1.2	3513	5	PCR-US92-11337-5 Sequence 5, Appli
17	35	1.2	6909	2	US-08-804-196-1 Sequence 1, Appli
18	35	1.2	6909	2	US-08-658-340-1 Sequence 1, Appli
19	35	1.2	6909	3	US-08-746-111-26 Sequence 26, Appli
C 20	34.6	1.2	1901	4	US-09-338-907-181 Sequence 181, App
C 21	34.6	1.2	56516	2	US-08-996-306-1 Sequence 1, Appli
C 22	34.6	1.2	56516	4	US-09-338-907-1 Sequence 1, Appli
C 23	34.6	1.2	56520	4	US-09-338-907-179 Sequence 179, App
C 24	34	1.2	486	4	US-09-328-111-363 Sequence 363, App
C 25	34	1.2	2689	1	US-08-465-795-2 Sequence 2, Appli
C 26	34	1.2	5589	1	US-08-465-795-1 Sequence 1, Appli
27	33.8	1.2	740	4	US-09-451-117-1 Sequence 1, Appli

28	33.4	1.2	8920	2	US-08-446-855A-1 Sequence 1, Appli
29	33.4	1.2	8920	4	US-09-150-741-1 Sequence 1, Appli
30	33.2	1.1	414	2	US-08-630-822A-63 Sequence 63, Appli
31	33.2	1.1	414	2	US-09-005-069-63 Sequence 63, Appli
32	33.2	1.1	2848	3	US-08-539-205A-3 Sequence 3, Appli
33	33.2	1.1	19124	2	US-08-487-826B-13 Sequence 13, Appli
34	33	1.1	660	1	US-07-991-867B-32 Sequence 32, Appli
35	33	1.1	660	2	US-08-107-755A-32 Sequence 32, Appli
36	33	1.1	660	2	US-08-544-332-32 Sequence 32, Appli
37	33	1.1	1511	1	US-07-991-867B-8 Sequence 8, Appli
38	33	1.1	1511	1	US-08-107-755A-8 Sequence 8, Appli
39	33	1.1	1511	2	US-08-544-332-8 Sequence 8, Appli
40	33	1.1	4810	3	US-08-852-629-11 Sequence 11, Appli
41	33	1.1	4838	3	US-08-852-629-15 Sequence 15, Appli
42	33	1.1	5658	4	US-08-881-450A-23 Sequence 23, Appli
43	32.6	1.1	2287	4	US-08-845-258-8 Sequence 8, Appli
44	32.6	1.1	2287	4	US-08-990-571-8 Sequence 8, Appli
45	32.6	1.1	2287	4	US-08-723-142A-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-915-107-3/c
Sequence 3, Application US/08915107
Patent No. 5885805
GENERAL INFORMATION:
APPLICANT: Burnham, Martin K.R.
APPLICANT: Lonetto, Michael A.
APPLICANT: Warren, Patrick V.
TITLE OF INVENTION: NOVEL Gbpa
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915.107
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50549-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-915-107-3
Query Match 1.4%; Score 40.6; DB 2; Length 1122;
Best Local Similarity 46.3%; Pred. No. 0.046;
Matches 133; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

Oy 1520 taacactgaagcatattgagatgaatcttctccatcttctgaagaagtgtgctgagatc 1579
Db 883 TAAATATGTTGATATCTTAATTAATTCATAAGTGTCTTAATTAATTCATCTCCTG 824
Oy 1580 cttatttg99tagagcctacaataacagaataactatacagacagactgagctta 1639
Db 823 GTTCTTCGATACCTTAATCTTTAAAGACATTTCTTTATCTTCATCATCTAATGAGCAA 764
Oy 1640 cctttcataagtgatgaataacatctccatcatgagatgactatggaattctcctatg 1699
Db 763 TTTCTTCTTCATTTTTCGACTAATAACATCATCTTCAGAGTCTTCTGCGTGCATATT 704
Oy 1700 aatccacagatctaacccatgctcgtctcatcaagcctatgctatct 1746
Db 703 CACGAATCGCTTTACTTTATCATATCATCATCACCAATTTCATCT 657

RESULT 4

US-09-273-613-1/C
Sequence 1, Application US/09273613
Patent No. 6203800
GENERAL INFORMATION:
APPLICANT: Burnham, Martin K.R.
APPLICANT: Lonetto, Michael A.
APPLICANT: Warren, Patrick V.
TITLE OF INVENTION: NOVEL Gbpa
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,107
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50549-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-273-613-1

Query Match 1.4%: Score 40.6; DB 4; Length 1125;
Best Local Similarity 46.3%; Pred. No. 0.048;
Matches 133; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

Oy 1460 atgagacagattctgagtgctataaataatggtgcaggaattctgctagcaatgcctcta 1519
Db 943 ATGAGGTCGACGTACATACCTGTTAAATGTCCAAACGACGTATCTTTCACACACGACG 884
Oy 1520 taacacgaagcatattgagatgaatcttctccatctctgaagaagtgtgctgagatc 1579

Db 883 TAAATATGTTGATATCTTAATTAATTCATAAGTGTCTTAATTAATTCATCTCCTG 824
Oy 1580 cttatttg99tagagcctacaataacagaataactatacagacagactgagctta 1639
Db 823 GTTCTTCGATACCTTAATCTTTAAAGACATTTCTTTATCTTCATCATCTAATGAGCAA 764
Oy 1640 cctttcataagtgatgaataacatctccatcatgagatgactatggaattctcctatg 1699
Db 763 TTTCTTCTTCATTTTTCGACTAATAACATCATCTTCAGAGTCTTCTGCGTGCATATT 704
Oy 1700 aatccacagatctaacccatgctcgtctcatcaagcctatgctatct 1746
Db 703 CACGAATCGCTTTACTTTATCATATCATCATCACCAATTTCATCT 657

RESULT 5

US-08-356-180-1
Sequence 1, Application US/08356180
Patent No. 5762924
GENERAL INFORMATION:
APPLICANT: DALL, DAVID J.
APPLICANT: FERNON, CAROL A.
APPLICANT: SRISKANTHA, ALAGACONE
TITLE OF INVENTION: RECOMBINANT ENTOMOPOXVIRUS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC AND BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,180
FILING DATE: 16-DEC-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MILLS, DEMETRA J.
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 1451-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
TELEX: AMERPAT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-356-180-1

Query Match 1.4%: Score 39.2; DB 1; Length 1560;
Best Local Similarity 48.6%; Pred. No. 0.14;
Matches 107; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Oy 783 ttctataacaatcgctgctttaaataatgtagaacaagcttctcagaagcttctgtag 842
Db 748 TTTGCACAAATATGTACTACCTAACAATTTATGCCGCCGAGCCGATGTTGGAGT 807
Oy 843 aggaagcaattaaatgaactactgccttagatggttaacagcaatcggtgtagatctttt 902
Db 808 AGTTCATTCCGAGATAGAGATGAGATGATTTTTCAGAGAAATTTGGTACTACCTTAT 867
Oy 903 tagtagacataatcacaanaattatggtgcgagctattatgagctctcctgtagtaccctagt 962

OY 1282 acagcctcgtatgatttccagagctacttcaatctgcagatttccacgaat 1341
DB 544 GCGCTTTTGCAGCAGTTTATGTTCTGTAGCGGATTTAGCAGATTACATTCGAATTA 603
OY 1342 ttacaacaaacacccgcacccctactctcagtaatggtttctatgtatcgaagt 1401
DB 604 AATCTTACAATAAAGGAGATGCAATTGCTCATTAAAGCTTCGGTTTATAGAGGCT 663

RESULT 8

US-08-584-760A-66
Sequence 66, Application US/08584760A
Patent No. 6290953
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Courtney, Michael G
APPLICANT: Fimlis, Christopher J A
APPLICANT: Sleep, Darrell
TITLE OF INVENTION: Medicine
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centeon L.L.C.
STREET: 1020 First Avenue
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,760A
CLASSIFICATION: 424
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/211,860
FILING DATE: 15-APR-1994
APPLICATION NUMBER: GB 9121815.6
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Naomi Biswas
REGISTRATION NUMBER: 38,384
REFERENCE/DOCKET NUMBER: 92H853-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610/878-4221
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1311
OTHER INFORMATION: /function= "figure 4"
NAME/KEY: CDS
LOCATION: 2..1311
US-08-584-760A-66

Query Match 1.2%; Score 36.2; DB 4; Length 1311;
Best Local Similarity 44.1%; Pred. No. 0.98; Mismatches 193; Indels 0; Gaps 0;
Matches 152; Conservative 0; Mismatches 193; Indels 0; Gaps 0;
OY 984 tataacatatcgcaataaaggaggcgtatctatatagacggaacgaagctc 1043
|||||

DB 364 TTAGATAAATTAGAAATCTATTCAGGTTTCCAGATATTTCACAGATGATACAGATTGAG 423
OY 1044 caaatcttcgcagccagccatgctatattttaaagaataatcttgactaatgtgaac 1103
DB 424 AGAATATTATTAAGATGTTGCTGTTGCTATTTAGTAAACTTCTTTAGCTCCAGC 483
OY 1104 taatgcaaatgtaaccagtaagctcagctcaatccctcctagaagaatgcaataacagtagc 1163
DB 484 TGATTAAGAATTTCTACGCTACTAGAGATATTACTGCTACTGTTGATTCTATTCATTAT 543
OY 1164 aagctcctcgtgtaaatctcattagagcagaggaagtagccaaatthaattttatga 1223
DB 544 TACTGCTTCTATTATTAGCTAAATAATTAGCTGAAGCTTAGATGCTTTAGTTATGATGT 603
OY 1224 tccattgaagttgcaatgcaagggtctctgctcctcaataagaagctgcaaac 1283
DB 604 TAAAGTTGCTTCTGCTGCTTTCATGCCAAGCTTAGCAATTAATCTGAAGCTTGCTGAAGC 663
OY 1284 agcctcgtatgatttccagagctacttcaatctgcagattt 1328
DB 664 GATCCTTGCTGCTGCTGCTAGCGGTGCTGTTAGAACTACTGCTTT 708

RESULT 9

US-07-828-788A-5
Sequence 5, Application US/07828788A
Patent No. 5273746
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIMANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIMANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: NA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3513 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: KENYAE
INDIVIDUAL ISOLATE: PS81F
IMMEDIATE SOURCE:
LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 81F
US-07-828-788A-5

Wed Apr 24 09:33:43 2002

us-09-677-752-1.rml

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 05:12:13 ; Search time 40.76 Seconds
(without alignments)
10652.069 Million cell updates/sec

Title: US-09-677-752-1

Perfect score: 2898

Sequence: 1 atgaaaaaaggttttctt.....aattgtctgcgattctag 2898

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 12861 seqs, 7490995 residues

Total number of hits satisfying chosen parameters: 257722

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New:*
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3: /cgn2_6/prodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/prodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48.4	1.7	1511	US-09-612-402A-10	Sequence 10, Appl
2	48.4	1.7	1515	US-09-612-402A-22	Sequence 22, Appl
3	48.4	1.7	4435	US-09-612-402A-1	Sequence 1, Appl
4	45.2	1.6	3324	US-09-612-402A-24	Sequence 24, Appl
5	42	1.4	3354	US-09-612-402A-23	Sequence 23, Appl
6	40.8	1.4	5621	US-09-630-630B-23	Sequence 23, Appl
7	40	1.4	3996	PCT-US02-06415-42	Sequence 42, Appl
8	38.2	1.3	9477	US-10-105-299-13241	Sequence 13241, A
9	38.2	1.3	9466	US-10-105-299-13242	Sequence 13242, A
10	37.4	1.3	282	US-09-789-189-553	Sequence 553, Appl
11	36.6	1.3	912	US-09-828-523A-19	Sequence 19, Appl
12	36.6	1.3	936	US-09-828-523A-85	Sequence 85, Appl
13	36.4	1.3	277	US-09-540-210B-15021	Sequence 15021, A
14	35.4	1.2	4205	US-10-105-299-13644	Sequence 13644, A
15	35.2	1.2	1481	US-10-105-299-2465	Sequence 2465, Ap
16	34.6	1.2	662	US-10-089-128-31	Sequence 31, Appl
17	34.2	1.2	4017	US-09-648-692B-10	Sequence 10, Appl
18	33.6	1.2	498	US-10-099-926-1619	Sequence 1619, Ap
19	33.2	1.1	12604	US-10-105-299-6697	Sequence 6697, Ap
20	33	1.1	298	US-09-685-209A-475	Sequence 475, Ap
21	33	1.1	2791	US-10-105-299-1300	Sequence 1300, Ap
22	33	1.1	2791	US-10-105-299-1301	Sequence 1301, Ap
23	33	1.1	2791	US-10-106-698-1534	Sequence 1534, Ap
24	32.8	1.1	16285	US-10-105-299-9034	Sequence 9034, Ap
25	32.8	1.1	16285	US-10-105-299-9035	Sequence 9035, Ap
26	32.4	1.1	789	US-09-540-209B-361	Sequence 361, Appl

27	32.4	1.1	17646	US-10-105-299-6422	Sequence 6422, Ap
28	32.4	1.1	17646	US-10-105-299-6424	Sequence 6424, Ap
29	32.2	1.1	294	US-09-540-210B-13065	Sequence 13065, A
30	32.2	1.1	6483	US-10-105-299-12426	Sequence 12426, A
31	32.2	1.1	6483	US-10-105-299-12427	Sequence 12427, A
32	32	1.1	6844	US-10-105-299-10429	Sequence 10429, A
33	32	1.1	6937	US-10-105-299-11722	Sequence 11722, A
34	32	1.1	13608	US-10-105-299-9203	Sequence 9203, Ap
35	32	1.1	12073	US-10-105-299-7267	Sequence 7267, Ap
36	32	1.1	22073	US-10-105-299-9014	Sequence 9014, A
37	32	1.1	22958	US-10-105-299-11723	Sequence 11723, A
38	32	1.1	40898	US-10-105-299-12480	Sequence 12480, A
39	31.8	1.1	231	US-09-540-210B-26664	Sequence 26664, A
40	31.8	1.1	11343	US-10-105-299-9409	Sequence 9409, Ap
41	31.8	1.1	11343	US-10-105-299-9411	Sequence 9411, Ap
42	31.6	1.1	474	US-10-097-105-435	Sequence 435, Ap
43	31.6	1.1	733	US-10-106-698-472	Sequence 472, Ap
44	31.6	1.1	2277	US-10-105-299-8237	Sequence 8237, Ap
45	31.6	1.1	2277	US-10-105-299-8238	Sequence 8238, Ap

ALIGNMENTS

RESULT 1
US-09-612-402A-10
Sequence 10, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 08/942,596
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 1511
TYPE: DNA
ORGANISM: Chlamydia sp.
US-09-612-402A-10

Query Match 1.7% Score 48.4 DB 5 Length 1511
Best Local Similarity 56.7% Pred. No. 0.0092
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 896 tcttttagtgaacatcacaaaaattatgacgagctattagctcctgtagta 955
Db 1007 tttcttagtagaagaatgctgctgctggaaggagcattatgacaaagctc 1066
QY 956 ccctagtgagataagccctacattataaacaatccatccaaatcttcgcgacgcacgtatttt 1015
Db 1067 cgttctgactactgagccctgtaacattttaaggaatcgtcgaatgat---ggtgag 1123
QY 1016 ctactatataagcagcaaccccaaaattcttcgcgacgcacgtatttt 1075
Db 1124 cgatttcttagaggaatctgagagctcgttattctgctgattatgagatatatt 1183
QY 1076 ttaatgaataatt 1089
Db 1184 ttagatgggaactct 1197

RESULT 2
US-09-612-402A-22
Sequence 22, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof

```

RESULT      8
US-10-105-299-13241/c
: Sequence 13241, Application US/10105299
:
: GENERAL INFORMATION:
:
: APPLICANT: Rosen, et. al
:
: TITLE OF INVENTION: Human Secreted Proteins
:
: FILE REFERENCE: 89950
:
: CURRENT APPLICATION NUMBER: US/10/105,299
:
: CURRENT FILING DATE: 2002-03-26
:
: NUMBER OF SEQ. ID NOS. 15197
:
: Prior Application removed - See File Wrapper or Patent
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 13241
:
: LENGTH: 9477
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
US-10-105-299-13241

```

QY 878 caggcaalcctgctgtcagatcttlttagtgacaataacaaaatttagcgagta 93
| | | | | | | | | | | | | | | | | | | | |
Db 187 CCGCAAGTTTGCTCTTTTTTGTAGTAATAATGTCAGACAAAATCTGCATT 122
| | | | | | | | | | | | | | | | | | | | |
QY 938 tttaagcttcigttagttaacctagtcggataatgcgccactctaatacaaatcgc 99
| | | | | | | | | | | | | | | | | | | | |
Db 127 TTTCTCTTAATATATGTGAATAATGTGGAAAGATGCAGATTTTAATCTTCATCAGCTAA 68
| | | | | | | | | | | | | | | | | | | | |
QY 998 ccaataaagaaggcgcatlctatlatagacggaacagcaactccaanaatt 1051
| | | | | | | | | | | | | | | | | | | | |
Db 67 GCTGGAACCTGACTTCTGCTAACC GGCTCTTTGGAACAATCACTCAACTT 14

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 04:43:58 ; Search time 1338.28 Seconds
(without alignments)
23269.619 Million cell updates/sec

Title: US-09-677-752-1

Perfect score: 2898
Sequence: 1 atgaaacacgctttctt.....aaattgctcgcattctag 2898

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*

- 1: em_estfun:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estom:*
- 5: em_estpl:*
- 6: em_estba:*
- 7: em_estro:*
- 8: em_estov:*
- 9: em_hlc:*
- 10: qb_estl:*
- 11: qb_est2:*
- 12: qb_hlc:*
- 13: qb_gss:*
- 14: em_gss_fun:*
- 15: em_gss_hum:*
- 16: em_gss_inv:*
- 17: em_gss_pln:*
- 18: em_gss_pro:*
- 19: em_gss_rtd:*
- 20: em_gss_vrt:*
- 21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	49.6	1.7	1101	13	CNS0039G
C 2	44.6	1.5	806	13	CNS04AEE
C 3	44	1.5	594	10	AM109947
C 4	44	1.5	1011	13	CNS0205x
C 5	43	1.5	968	13	CNS006R5
C 6	41.6	1.4	538	13	AZ068468
C 7	41.4	1.4	1101	13	CNS0182P
C 8	41.2	1.4	667	11	BF298817
C 9	40.6	1.4	1101	13	CNS017DP
C 10	40.6	1.4	891	13	AZ529319
C 11	40.4	1.4	919	13	AZ659216
C 12	40.4	1.4	573	13	A0981798

C 13	40.2	1.4	487	13	AZ900612
C 14	40.2	1.4	562	13	PT013K11R
C 15	40	1.4	493	13	AA550487
C 16	39.8	1.4	324	11	F07305
C 17	39.8	1.4	350	10	A0060746
C 18	39.8	1.4	388	10	A1831292
C 19	39.8	1.4	420	10	AJ280396
C 20	39.6	1.4	409	10	BE580247
C 21	39.6	1.4	603	13	AQ439611
C 22	39.6	1.4	1101	13	CNS00GDR
C 23	39.4	1.4	306	10	AA094179
C 24	39.4	1.4	596	13	AQ0803690
C 25	39.2	1.4	410	11	BE834190
C 26	39.2	1.4	685	11	BF276133
C 27	39.2	1.4	801	11	C24332
C 28	39.2	1.4	894	13	AZ529017
C 29	39.2	1.4	1074	13	CNS07E9K
C 30	39	1.3	625	13	AZ432433
C 31	39	1.3	863	13	AZ534809
C 32	39	1.3	867	13	AZ539614
C 33	39	1.3	875	13	AZ534004
C 34	39	1.3	881	13	AZ532395
C 35	39	1.3	891	13	AZ685903
C 36	39	1.3	917	13	AZ550269
C 37	39	1.3	940	13	AZ680393
C 38	39	1.3	946	13	AZ683083
C 39	39	1.3	1101	13	CNS00CSN
C 40	38.8	1.3	391	10	A1419477
C 41	38.8	1.3	419	10	A1453440
C 42	38.8	1.3	450	10	BE710020
C 43	38.8	1.3	480	11	BF610746
C 44	38.8	1.3	579	10	A0038989
C 45	38.8	1.3	762	13	CNS038UC

ALIGNMENTS

RESULT 1
CNS0039G/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

CNS0039G 1101 bp DNA
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL063921.1 GI:4941778
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osoegawa and
Aaron Mammosier in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2: cn bw sp, the same strain used for the BGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Tel: 608 262 2024
Fax: 608 262 2824

Email: bradfield@oncology.wisc.edu
This clone was sequenced as part of a project to develop a database on gene expression changes following exposure to various environmental toxicants. The database can be accessed at <http://mcardsle.oncology.wisc.edu/bradfield/>. Treatment- Dioxin (10 ug/kg, ip) in a dioxane vehicle. Animals sacrificed 48 hrs post-injection.

FEATURES

Source

```

SOURCE
1. 354
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_1p="MT16306"
/clone_1p="mouse liver, dioxin treated"
/sex="male"
/lab_host="JM109"
/note="Organ: liver; Vector: pGEM11zf (Promega); Site:1;
NotI; Site:2; EcoRI: First strand cDNA was primed with a
NotI-polyT primer
[5'-AAGCTGAGACAAATTCGCGCGCCGACAGAAATTTTCTTTTCTTTT-3']
Double-stranded cDNA was ligated with EcoRI adapters
(Pharmacia), digested with NotI, and ligated into the
EcoRI/NotI sites of the pGEM11zf vector. The library was
NOT normalized."
156 a 136 c 130 g 172 t

```

BASE COUNT	156 a	136 c	130 g	172 t
ORIGIN				
Query Match		1.58;	Score 44;	DB 10; Length 594;
Best Local Similarity		53.58;	Pred. No. 1;	
Matches 92; Conservative		0;	Mismatches 80;	Indels 0; Gaps 0

RESULT 4

LOCUS	1011 bp	DNA	GSS	12-MAY-2000
DEFINITION	Tetradon nigroviridis genome survey sequence T7 end of clone 22J14 of library G from Tetradon nigroviridis, genomic survey sequence.			

AUTHORS

TITLE Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
motif-based microarrays and DNA sequence

JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1011)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT	This sequence is a single read and was generated as part of a large scale second generation project of the Terodon nigrivittatus

FEATURES

Source

```

source
1. 1011
/organism="Tetradodon n1groviridis"
/db_xref="taxon:99883"
/clone="21j14"
/clone_11b="G"
/note="Genoscope sequence ID : C0AC221DE07LPI-end : T7
316 a 216 c 176 g 301 t 2 others
BASE COUNT
ORIGIN

```

Query Match	1.5%	Score 44	DB 13	length 1011
Best Local Similarity	52.1%	Pred. No. 1.1		
Matches 98	Conservative	0	Mismatches 90	Indels 0
			Gaps	0

RESULT 5

CHROMOSOME	LOCUS	COORDINATES	GENE	FEATURES
CNS006f5	968 bp	DNA	GSS	03-JUN-1999
Drosophila melanogaster	genome survey sequence	TE13 end of BAC t		
BAC141419 of RP11-98	library from Drosophila melanogaster (fruit fly), genomic survey sequence.			

REFERENCE

TITLE	COMMENT
<p>Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage BP 191 91006 Evry cedex - FRANCE (E-mail : secref@genoscope.cns.fr Web : www.genoscope.cns.fr)</p>	<p>determination of this BAC-end sequence was carried out as part of a</p>

COMMENT

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```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPC1-24-150H6"
/clone_lib="RPC1-24"
/sex="Male"
/cell_type="Spleen/Brain"
/notes="Vector: pTARBAC1; site_1: BamHI; site_2: BamHI;
RPC1-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

```

BASE COUNT 147 a 85 c 108 g 147 t

ORIGIN

Query Match 1.48; Score 40.2; DB 13; Length 487;
 Best Local Similarity 57.68; Pred. No. 10;
 Matches 72; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY 804 taaaatgtagaacagctcttcagaagctctgtatgagagcaattaagtaactac 863
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 355 TAAAAATTTGAACTATATCTCATATGCTTTTGTGAGAGCTGCACTACAGGCACTTT 296
 OY 864 tcgcctagatgtaccagcgaatcgtgtagatcttctttagtgcataatcacaacaaa 923
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 295 TGCCCTAGTTTGCAAGCGGAAAAAATTATGAGCTCTTAGAACACGCAATAGATACAGAA 236
 OY 924 ttatg 928
 |||||
 DB 235 TAAAG 231

RESULT 14

PT013K11R 562 bp DNA GSS 13-JUL-2001
 LOCUS Parametrium tetraurelia sequence R13F06 of the end of plasmid
 DEFINITION PT013K11, genomic survey sequence.

ACCESSION AL446148
 VERSION AL446148.1 GI:11123039
 KEYWORDS GSS.

SOURCE Parametrium tetraurelia.
 ORGANISM Parametrium tetraurelia.

REFERENCE 1 (bases 1 to 562)
 AUTHORS Keliier,A.M. and Cohen,J.
 TITLE An indexed genomic library for Parametrium complementation cloning
 JOURNAL J. Eukaryot. Microbiol. 47 (1), 1-6 (2000)

REFERENCE

2 (bases 1 to 562)
 AUTHORS Dessen,P., Zagulski,M., Gromadka,R., Plattner,H., Kismehl,R.,
 Meyer,E., Betermier,M., Schultze,J.E., Linder,J., Pearlman,R.E.,
 Kunz,C., Potney,J.J., Satir,B.H., Van Houten,J.L., Keller,A.M.,
 Foisassard,M., Sperling,L. and Cohen,J.
 TITLE Parametrium genome survey: a pilot project
 JOURNAL Trends Genet. 17 (6), 306-308 (2001)

REFERENCE

3 (bases 1 to 562)
 AUTHORS Wong,L. and Pearlman,R.E.
 TITLE Random sequencing of the Parametrium macronuclear genome
 JOURNAL Core Molecular Biology Facility, York University, 4700 Keele St.,
 Toronto, Canada M3J 1P3
 4 (bases 1 to 562)
 Cohen,J. and Sperling,L.
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-2000) Parametrium Genome Survey Project, Centre de
 Genetique Moleculaire, Centre National de la Recherche
 Scientifique, 91198 Gif-sur-Yvette, France. E-mail:
 sperling@cm.cnr-sg.fr

REFERENCE

562
 The present survey of the Parametrium tetraurelia macronuclear
 genome consists of end sequences of a library of random 4-12 kb
 fragments obtained by Sau3a partial digestion of macronuclear DNA

REFERENCE

562
 The present survey of the Parametrium tetraurelia macronuclear
 genome consists of end sequences of a library of random 4-12 kb
 fragments obtained by Sau3a partial digestion of macronuclear DNA

COMMENT

Cloned in the BamHI site of pBSIIKS-. See [4].
 Genes are predicted from matches to other sequences. For more
 information about this sequence of the Parametrium Project, see
 http://parametrium.cgm.cnr-sg.fr.
 Location/Qualifiers

FEATURES

1..562

/organism="Parametrium tetraurelia"

/macronuclear

/strain="stock d4-2"

/db_xref="taxon:5888"

BASE COUNT 271 a 58 c 68 g 165 t

ORIGIN

Query Match 1.48; Score 40.2; DB 13; Length 562;
 Best Local Similarity 54.48; Pred. No. 10;
 Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

OY 965 ataagcgccctactactattataacacatctgcacataaagggggcgctactata 1024
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 187 ATATACCAATTAACACGCAATTAACATTAATTAATTAACACGCAATTAACATA 246
 OY 1025 tagacggaaccagcaactccaaattctgcgagccgcatgtatatttaagaaa 1084
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 247 ATTATACCAACGCAATTAACATTAATTAACATTAATTAACATTAATTAATTAATA 306
 OY 1085 atattgactaatgtactaatgcaaat 1113
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 307 ATATATACCAATTAATTAATTAATTAACCTCAAT 335

RESULT 15

AA550487 493 bp DNA GSS 05-DEC-2000
 LOCUS 1642m3 gmbPFHB3.1, G. Roman Reddy plasmodium falciparum genomic
 clone 1642m. DNA sequence.
 DEFINITION AA550487
 ACCESSION AA550487.1 GI:2320739
 VERSION AA550487.1 GI:2320739
 KEYWORDS GSS.

SOURCE malaria parasite P. falciparum.
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 493)
 AUTHORS Dame,J.B., Annot,D.E., Bourke,P., Chakrabarti,D., Christodoulou,Z.,
 Coppel,R., Cowman,A., Craig,A., Fischer,K., Foster,J., Goodman,N.,
 Hinterberg,K., Holder,A.A., Holt,D., Kemp,D., Lanzer,M., Lim,A.,
 Newbold,C., Ravetch,J.V., Reddy,G.R., Rubio,J., Schuster,S.M., Su
 X.-Z., Thompson,J.K., Vitali,F., Wellens,T.E. and Werner,E.
 TITLE Current status of the Plasmodium falciparum genome project
 JOURNAL Mol. Biochem. Parasitol. 79, 1-12 (1996)

REFERENCE

97001675
 CONTACT: Dame JB
 DEPT. OF Pathobiology, College of Veterinary Medicine
 University of Florida
 2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
 Tel: 352 392 4700
 Fax: 352 392 9704
 Email: damej@mail.ufl.edu
 Seq primer: T3
 Class: shotgun.

COMMENT

Location/Qualifiers
 1..493
 /organism="Plasmodium falciparum"
 /db_xref="taxon:5833"
 /clone="1642m"
 /clone_lib="gmbPFHB3.1, G. Roman Reddy"
 /lab_host="E. coli XL1-Blue"
 /notes="Vector: pBluescript SK(+); Genomic DNA, from
 asynchronous blood stage parasites of the cloned Honduran
 HB3 isolate cultured in vitro, was digested with mung bean
 nuclease in the presence of 30% formamide at 50°C (Vernick
 K.D., Imberiski, R.B., and McCutchan, T.F. 1988. Nucleic
 Acids Research 16:6883-6896). The ends of the fragments

FEATURES

Source

Oy	2236	gagcgcttcacgaagaacaacgcgtactcctctaanaattcatgccaaaggagaatgctc	2295
Db	836	BAYMCACTTAALYIMRRRAWIGTATTTKKAYLAALWDAIKMGACACAAGADATTTHAY	777
Oy	2296	tctcatatgcgaagaaggtcttgcctgcataaattagtggacctcacgctatagagac	2355
Db	776	TCCYTTTTTTTAMATTTTTTTTTTTATMGCATTTTWTFHYTDAAHAAAANKAAGAW	717
Oy	2356	cataactctccaccattctctatatcccgaagagagaatctaacctctcaaggagacgtccg	2414
Db	716	AMGAMMACCTWCACAGKATATACAAKCBGDMAAATASSCATCAGAGSGKWMTTYCMCG	658
RESULT	10		
LOCUS	AZ529319/c		
DEFINITION	AZ529319	891 bp	DNA
ACCESSION	ENTBRK8TR	Entamoeba histolytica	Sheared DNA Entamoeba histolytica genomic, DNA sequence.
VERSION	AZ529319		
KEYWORDS	AZ529319.1	GI:11082075	GSS.
SOURCE	Entamoeba histolytica.		
ORGANISM	Entamoeba histolytica		
REFERENCE	Eukaryota; Entamoebidae; Entamoeba.		
AUTHORS	Loftus, B., Van Aken, S. and Fraser, C.		
TITLE	1 (bases 1 to 891)		
JOURNAL	Determination of clone end sequences from Entamoeba histolytica HMI-IMSS sheared DNA library		
COMMENT	Unpublished (2000) Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: entae@ligr.org Clones are derived from the Entamoeba histolytica HMI-IMSS sheared DNA library Seq primer: M13-Reverse Class: Shotgun High quality sequence start: 33 High quality sequence stop: 793. Location/Qualifiers 1..891		
FEATURES			
Source			

BASE COUNT	272 a	148 c	68 g	403 t
ORIGIN				
Query Match	14%	Score 40.6:	DB 13:	Length 891:
Best Local Similarity	46.1%:	Pred No. 8.7:	Mismatches 159:	Gaps 0
Matches 156:	Conservative	0:	Indels	0:
Oy	1068	tattatctttaagaaacatcgtgactaatgcgaatcgaatcaccagtccgc	1127	
Dd	776	TTTAAATTAAGGATTAATGTGGACATAAATAAGTTAAAGCATATTATGTGA	717	

Dy	1128	agcgaaccctccctgaaagaatgcataacgttcgaagccctccctcgtagaatctatt	1187
Dy	716	AGAAATAATCTATTATTAATAAAGACAAAAAAGACAAATTAAAGAGAGGAATTTATGT	657
Dy	1188	aggagcaggagagtagcccaaatctaatttcttatgatccctatlgaaagttaacatgcagg	1247
Dy	656	TGGAGAAGTATTGTTGTTATTAATACAAAAGAAATTTAAATTAAGTATTAAATTAAGGAAA	597
Oy	1248	ggctctcgtgccttcataaggaagcgcgatalccaacagcctcgagatatttcaggagc	1307
Dy	596	TAGAATACGATATATTCCTATTGTTGATATAGTAATCTTTTAAATCCATTTCCAGAGA	537
Oy	1308	tactgttaattccagatlttcatacgaaccttacaaaacaaaaaacatgcgtca	1362
Dy	536	TTATTTCAAAATATGGAATATATTATTAATGATGATGACTTTCATATTAACCGGAA	482
RESULT	11		
LOCUS	A2669216/c		
DEFINITION	A2669216	919 bp DNA	GSS
VERSION	ENHHP96TR	Entamoeba histolytica Sheared DNA	Entamoeba histolytica
KEYWORDS	A2669216	genomic, DNA sequence.	
SOURCE	A2669216.1	GI:11806362	GSS.
ORGANISM	Entamoeba histolytica.		
REFERENCE	1 (bases 1 to 919)	Loftus,B., Van Aken,S. and Fraser,C.	Determination of clone end sequences from Entamoeba histolytica HM1:IMSS sheared DNA library Unpublished (2000)
JOURNAL COMMENT	Contact: Brendan J Loftus		
	Department of Eukaryotic Genomics		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 0200		
	Fax: 301 838 0208		
	Email: entae@ligr.org		
	Clones are derived from the Entamoeba histolytica HM1:IMSS sheared		
	DNA library		
	Seq primer: M13-Reverse		
	Class: shotgun		
	High quality sequence start: 22		
	High quality sequence stop: 803.		
	Location/Qualifiers		
	1..919		

BASE COUNT	319 a	105 c	128 g	367 t
ORIGIN				
Query Match		14%	Score 40.6	DB 13
Best Local Similarity		49.8%	Pred No. 8	7
Matches 103		Conservative	0	Mismatches 104
				Indels 0
				Gaps 0


```

RESULT 14
US-10-105-299-13644/c
: Sequence 13644, Application US/10105299
:
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al
: TITLE OF INVENTION: Human Secreted Proteins
: FILE REFERENCE: PS950
: CURRENT APPLICATION NUMBER: US/10/105,299
: CURRENT FILING DATE: 2002-03-26
: NUMBER OF SEQ ID NOS: 15197
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 13644
:
: LENGTH: 4205
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
US-10-105-299-13644

```

	Query Match	Similarity	1.2%	Score	35.4	DB	6	Length	4205
Best Local	Similarity	59.4%		Pred. No.	16				
Matches	60	Conservative	0	Mismatches	41	Indels	0	Gaps	0
OY	2177	tacgagcgacagacacacaccttctatctgaatctcgtctagacctctaccaccaactcaatg	2236						
Db	3761	ttacacggatgacacatcncacattctcttcttcttatacctgaataatcncacataatataata	3702						
OY	2237	agcgcttacgcgaataaacaacgctatctctctcaataattactca	2277						
Db	3701	ggcacttaaacatattatagaataacattttcttataatatatttga	3661						

```

RESULT 15
US-10-105-299-2465/C
; Sequence 2465, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2465
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-2465

```

[illegible]

```

Query Match      1.3% ; Score 38.2; DB 6; Length 9477;
Best Local Similarity 52.1%; Pred. No. 4.2;
Matches    85; Conservative   0; Mismatches     78; Indels       0; Gaps        0;

Oy 1304 gagctactgtaattcgtcgagatlttcataacgcgaatltaacaacaaaaccctggcac 1363
    ||| |||| |
Db 8408 GATAAATTTCGATTTCACTTGAACATTTCTTAAGCAGAATTTGGAGTAACATCCAGTTT 8349
|||||

Oy 1364 cccctaactcagaatgytgtttcatgatcgaagaatcaagtcttagtaagaaac 1423
    ||| |||| |
Db 8348 ATCTTCCTTGACTAATCACGTGCCCTGTAAAGCACAATCATAACACAGCAGTAGTAAGT 8289
|||||

Oy 1424 gattcacacaacctggggtgttgtctctctgaggaaatggagc 1466
    ||| |||| |
Db 8288 GAATGATGAATAATAGAGCATTTTGATNACGTAAGAAAACAGTGC 8246
|||||

RESULT          9
US-10-105-299-13242/c
Sequence 13242, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P5950
CURRENT APPLICATION NUMBER: US/10/105,299
PRIORITY FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13242
LENGTH: 9496
TYPE: DNA
ORGANISM: Homo sapiens
US-10-105-299-13242

Query Match      1.3%; Score 38.2; DB 6; Length 9496;
Best Local Similarity 52.1%; Pred. No. 4.2;
Matches    85; Conservative   0; Mismatches     78; Indels       0; Gaps        0;

Oy 1304 gagctactgtaattcgtcgagatlttcataacgcgaatltaacaacaaaaccctggcac 1363
    ||| |||| |
Db 8427 GATAAATTTCGATTTCACTTGAACATTTCTTAAGCAGAATTTTGAGTAACATCCAGTTT 8368
|||||

Oy 1364 cccctaactcagaatagytttctatgatcalcgaagaatcgtcagcttacagtgaac 1423
    ||| |||| |
Db 8367 ATTCTTCCTTGACTAATCACGTGCCCTGTAAAGCACAATCATAACACAGCAGTAGTAAGT 8308
|||||

Oy 1424 gattcacacaacctggggtgttgtctctctgaggaaatggagc 1466
    ||| |||| |
Db 8307 GAATGATGAATAATAGAGCATTTTGATNACGTAAGAAAACAGTGC 8265
|||||

RESULT         10
US-09-789-189-553
Sequence 553, Application US/09789189
GENERAL INFORMATION:
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: Human Polynucleotides and Polypeptides
FILE REFERENCE: 25436/1720
CURRENT APPLICATION NUMBER: US/09/789,189
PRIORITY FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/183452
PRIORITY FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 2005
SOFTWARE: PatentIn version 3.1
SEQ ID NO 553
LENGTH: 262
TYPE: DNA
ORGANISM: Homo sapiens
US-09-789-189-553
```

```

Query Match 1.3%: Score 37.4; DB 5; Length 262:
Best Local Similarity 57.1%: Pred. No. 2.5:
Matches 69: Conservative 0; Mismatches 51; Indels 0; Gaps 0:

QY 123 aaataaattagttgcagagagacactcaatctcaactaactgctatctgataact 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 54 aaaaatttccttcttactactaacatccacccaacaaactctcccaaaccc 113

OY 183 acgtaactactgctcttctacaaaaaacctcccaagaagagctgctgcacaa 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 actacacttttaacttaaaaaaaalttaccatcaaaaaltcaacttcaaaaaa 172

RESULT 11
US-09-828-523A-19/c
: Sequence 19, Application US/09828523A
: GENERAL INFORMATION:
: APPLICANT: The Pharmacia & Upjohn Company
: TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
: FILE REFERENCE: 268.62120101
: CURRENT APPLICATION NUMBER: US/09/828.523A
: CURRENT FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/286,327
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 19
: LENGTH: 912
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
US-09-828-523A-19

Query Match 1.3%: Score 36.6; DB 5; Length 912:
Best Local Similarity 51.5%: Pred. No. 5.5:
Matches 84: Conservative 0; Mismatches 79; Indels 0; Gaps 0:

QY 330 tgcgagtcaccaatctctccacgctgagagatcgtgatcaataagtcctgtaacttga 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 TGCAATTGCCACTTTCTTTAGATGATGATTCCTTGTCATCAACTCTACAATTGAG 142

OY 390 aaataaactctgtgcagaccatttactatcgagtaattcctatgcagctgtataaat 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 CAATTAACCTGCTGCTAGATTATCTACACAAAATATCCCTGCTCTTAACAATTGAAT 82

OY 450 aagaagagcgagccattcatgctcaaatcttactataat 492
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 AACCAAGATTACTGCGCCAGATAAACCTGTTACAACTAAT 39

RESULT 12
US-09-828-523A-85/c
: Sequence 85, Application US/09828523A
: GENERAL INFORMATION:
: APPLICANT: The Pharmacia & Upjohn Company
: TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
: FILE REFERENCE: 268.62120101
: CURRENT APPLICATION NUMBER: US/09/828.523A
: CURRENT FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/266,327
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 85
: LENGTH: 936
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Nucleotide sequence of S. aureus coding region cloned for expr
US-09-828-523A-85

```

```
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 08/942,596
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1515
TYPE: DNA
ORGANISM: Chlamydia sp.
US-09-612-402A-22
```

```
Query Match          1.7%: Score 48.4; DB 5; Length 1515;
Best Local Similarity 56.7%: Pred. No. 0.0092;
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;
```

```
QY 896 tcttttttagtgcacatacacaaaaattatgctgcgagctatttaccgtcctctagta 955
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 1007 ttctcttagtagcaatgtagctgctgggaaggagctatttaccgcaaaagctct 1066
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
QY 956 cccctagtgataatgcccctactacttataacaatatcgccataataagggggagcg 1015
      ||| ||| ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| |||
DB 1067 cggctgctaactgtgcccctgtacaaatttctaaggaataatcgctatgat--gg 1123
      ||| ||| ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| |||
QY 1016 ctatctatagacggaaccgaactccaattcttgcgacgcgcatgtattatt 1075
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 1124 cgatttatttaggaagaactctggagagccagtttactctgctgataatgagatatatt 1183
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
QY 1076 ttaatgaaataatt 1089
      ||| ||| ||| |||
DB 1184 tcgatgggaactct 1197
      ||| ||| ||| |||
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RESULT 3

```
US-09-612-402A-1
Sequence 1, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
APPLICANT: Pace, John
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 08/942,596
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 4435
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression Vector
NAME/KEY: CDS
LOCATION: (382)..(3417)
OTHER INFORMATION:
US-09-612-402A-1
```

```
Query Match          1.7%: Score 48.4; DB 5; Length 4435;
Best Local Similarity 56.7%: Pred. No. 0.012;
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;
```

```
QY 896 tcttttttagtgcacatacacaaaaattatgctgcgagctatttaccgtcctctagta 955
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 1472 ttctcttagtagcaatgtagctgctgggaaggagctatttaccgcaaaagctct 1531
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
QY 956 cccctagtgataatgcccctactacttataacaatatcgccataataagggggagcg 1015
      ||| ||| ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| |||
DB 1532 cggctgctaactgtgcccctgtacaaatttctaaggaataatcgctatgat--gg 1588
      ||| ||| ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| |||
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QY 1016 ctatctatagacggaaccgaactccaattcttgcgacgcgcatgtattatt 1075
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 1589 cgatttatttaggaagaactctggagagccagtttactctgctgataatgagatatatt 1648
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
QY 1076 ttaatgaaataatt 1089
      ||| ||| ||| |||
DB 1649 tcgatgggaactct 1662
      ||| ||| ||| |||
```

RESULT 4

```
US-09-612-402A-24
Sequence 24, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
APPLICANT: Pace, John
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 08/942,596
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 3324
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression Vec
US-09-612-402A-24
```

```
Query Match          1.6%: Score 45.2; DB 5; Length 3324;
Best Local Similarity 55.7%: Pred. No. 0.067;
Matches 108; Conservative 0; Mismatches 83; Indels 3; Gaps 1;
```

```
QY 896 tcttttttagtgcacatacacaaaaattatgctgcgagctatttaccgtcctctagta 955
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 1094 ttctcttagtagcaatgtagctgctgggaaggagctatttaccgcaaaagctct 1153
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
QY 956 cccctagtgataatgcccctactacttataacaatatcgccataataagggggagcg 1015
      ||| ||| ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| |||
DB 1154 cggctgctaactgtgcccctgtacaaatttctaaggaataatcgctatgat--gg 1210
      ||| ||| ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| |||
QY 1016 ctatctatagacggaaccgaactccaattcttgcgacgcgcatgtattatt 1075
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
DB 1211 cgatttatttaggaagaactctggagagccagtttactctgctgataatgagatatatt 1270
      ||| ||||| ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| |||
QY 1076 ttaatgaaataatt 1089
      ||| ||| ||| |||
DB 1271 tcgatgggaactct 1284
      ||| ||| ||| |||
```

RESULT 5

```
US-09-612-402A-23
Sequence 23, Application US/09612402A
GENERAL INFORMATION:
APPLICANT: Jackson, W. James
APPLICANT: Pace, John
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 7969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 08/942,596
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 3354
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Db 868 TCCTTGTAGTACACCAATCTAGAGCTAGATTGGAATTTTCTCTACTGC 927
Oy 963 gataatgcccactactacttataacatagcgaat 1002
Db 928 TGTTCATGATCTAGCTATTATGAGTTTATATCAATAAT 967

RESULT 6
US-08-718-905-1
Sequence 1, Application US/08718905
Patent No. 6063736

GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Donovan, Judith C.
APPLICANT: Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34
TITLE OF INVENTION: COMPOSITIONS AND USES THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,905
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-718-905-1

Query Match 1.3%: Score 38.4; DB 3; Length 807;
Best Local Similarity 46.1%: Pred. No. 0.17; Indels 3; Gaps 1;
Matches 166: Conservative 0; Mismatches 191; Indels 3; Gaps 1;

Oy 1045 aaatttcgcgcagccatgctatattttaaataatgtgactaagttaact 1104
Db 304 AAATTGGTTTGTAACTCGATGTTACTTTAAAGGTATCAGCAATATATATAGT 363
Oy 1105 aatgaatgtaccagtagcagtaactccctcctagaagaataatgaataagtagca 1164
Db 364 ACAACAATATACACTACAAACAACACACACCTGTCAGATTCAACAAAGTAACT 423
Oy 1165 agctcctctgtgaatctctatagagcagggagtagcgaataatatttaattatgat 1224
Db 424 ATTCCTCCAAACTTATATGTGAGGCTGCTATGATTAATCCAAATGGAACATATATGTT 483
Oy 1225 cc---tatgaagtagcaatgcaagggtctctgtgctccctcaataaagaagctgataca 1281
Db 484 CCGGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
Oy 1282 acagagctctgtagtatttctcagagctactgttaattctgcagatttcatcaagcaat 1341
Db 544 GCGTTATATGACGAGATTATGTTCTGTAGCGGATTAGCAGATTACAAATCAATTTTA 603

Oy 1342 ttacaacaaaacaccctgaccccttactctcagtaatggtttctatglatcgaagt 1401
Db 604 AATCTTACAAATTAAGGGGATGGAATGCTCACTTTAAAGGTTGGGTTTATAGAGGTT 663

RESULT 7
US-09-550-497-1
Sequence 1, Application US/09550497
Patent No. 6248536

GENERAL INFORMATION:

APPLICANT: Donovan, William P.
APPLICANT: Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34
TITLE OF INVENTION: COMPOSITIONS AND USES THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,497
FILING DATE: 14-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/718,905
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-550-497-1

Query Match 1.3%: Score 38.4; DB 4; Length 807;
Best Local Similarity 46.1%: Pred. No. 0.17; Indels 3; Gaps 1;
Matches 166: Conservative 0; Mismatches 191; Indels 3; Gaps 1;

Oy 1045 aaatttcgcgcagccatgctatattttaaataatgtgactaagttaact 1104
Db 304 AAATTGGTTTGTAACTCGATGTTACTTTAAAGGTATCAGCAATATATATAGT 363
Oy 1105 aatgaatgtaccagtagcagtaactccctcctagaagaataatgaataagtagca 1164
Db 364 ACAACAATATACACTACAAACAACACACACCTGTCAGATTCAACAAAGTAACT 423
Oy 1165 agctcctctgtgaatctctatagagcagggagtagcgaataatatttaattatgat 1224
Db 424 ATTCCTCCAAACTTATATGTGAGGCTGCTATGATTAATCCAAATGGAACATATATGTT 483
Oy 1225 cc---tatgaagtagcaatgcaagggtctctgtgctccctcaataaagaagctgataca 1281
Db 484 CCGGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543

Oy	1460	atgagcagcgttcctgagttgctctaaataatggcgaggaattctgcctagcaatgcctta	1519
Db	943	ATTGAGGTGGAGTCATACCTTGTTTAAATGTCACAGACGTACTCTTGACACACGACG	884
Oy	1520	taacacccgaagcatalatgatatgaactcttcctccatcttcgaaagtggtgcctgattc	1579
Db	883	TAAATATGTTGATTAATCCTTAATTAATTCATTAAGTTGTCTAATTAATGACATTAATCCTG	824
Oy	1580	cttatctggtgttagagccctaaataataagaacatactacatacagaatagctgaagta	1639
Db	823	GTTTGTGGATACCTAAATCTCTTAAGAGACTTTCTTAATCTTATCATCATTAATGACGA	764
Oy	1640	cccttcattaaatgatatgaataaactccatcaatctatgatctatggaattctccatg	1699
Db	763	TTTCTCTTTCATATTTTGGACATATAACATCACTCAAGACTCTCTCTGCGTCGATATT	704
Oy	1700	aatccacagatctaacccaagctctgcgcatacnaagcctatgctact	1746
Db	703	CACGAATCGCTTTTACTTTATCATTAATCATCATCACCAATTTTCATT	657

```

1      RESULT 2
2      US-09-273-613-3/C
3      Sequence 3, Application US/09273613
4      Patent No. 6203800
5      GENERAL INFORMATION:
6      APPLICANT: Burnham, Martin K.R.
7      APPLICANT: Lonetto, Michael A.
8      APPLICANT: Warren, Patrick V.
9      TITLE OF INVENTION: NOVEL Gbpa
10     NUMBER OF SEQUENCES: 7
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Dechert Price & Rhoads
13     STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
14     CITY: Philadelphia
15     STATE: PA
16     COUNTRY: US
17     ZIP: 19103
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Diskette
20     COMPUTER: IBM Compatible
21     OPERATING SYSTEM: DOS
22     SOFTWARE: FastSEQ for Windows Version 2.0
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/09/273,613
25     FILING DATE:
26     CLASSIFICATION:
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: 08/915,107
29     FILING DATE:
30     ATTORNEY/AGENT INFORMATION:
31     NAME: Dickinson, Todd Q
32     REGISTRATION NUMBER: 28,354
33     REFERENCE/DOCKET NUMBER: P5049-4
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: 215-994-2252
36     TELEFAX: 215-994-2222
37     TELEX:
38     INFORMATION FOR SEQ ID NO: 3:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 1122 base pairs
41     TYPE: nucleic acid
42     STRANDEDNESS: double
43     TOPOLOGY: linear
44     US-09-273-613-3

```

Query Match	1.48;	Score 40.6;	DB 4;	Length 1122;
Best Local Similarity	46.38;	Pred. No. 0.048;		
Matches 133;	Conservative	0;	Mismatches 154;	Indels 0;
			Gaps	

0Y	1460	atgagacagttctgagttgctataaaatggtgcaggaattctctgacgaatgcctcta	1519

Db	943	ATTGAGTGGACGATCAATACCTGTTTAATGATCGAAGCAGCTACTCTTGCAACCCAGCAG	884
QY	1520	taaacctggaacgacatctgtaataacctcttcacatcttgaaaagtgctgagtc	1579
Db	883	TAAATATGTTGGTATATCCATAATATTCATATAGTTGTTTATATGATCAATATCTG	824
QY	1580	cttatctgtggtagagcccaacaatacagcaatacatalacagcagctactgcagta	1639
Db	823	GTTTGTGCATACCTAAATCTTCTTAAGACACTTTCTTATCTTCATCAATCATATATGAGCA	764
QY	1640	cccttctcattaaagtagatgtaaaaactcctcactatgtagaactaagtggaattctcctatg	1699
Db	763	TTTCTTCTTAATTTTTGGCACTAATAACATCACTTCAGAGCTCTTTCGGCTGCATATT	704
QY	1700	aatcacagatctaacccacagcctctcaccacagcctctgcatc	1746
Db	703	CAGCAATGCGCTTTTACTTTATTCATATATCATATCAATCAACCAATTTTCATCT	657

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1  US-08-915-107-1
2  RESULT 3
3  US-08-915-107-1/c
4  Sequence 1, Application US/08915107
5  Patent No. 585805
6  GENERAL INFORMATION:
7  APPLICANT: Burnham, Martin K.R.
8  APPLICANT: Lonetto, Michael A.
9  APPLICANT: Warren, Patrick V.
10 TITLE OF INVENTION: NOVEL Gbpa
11 NUMBER OF SEQUENCES: 7
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Dechert Price & Rhoads
14 STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
15 CITY: Philadelphia
16 STATE: PA
17 COUNTRY: US
18 ZIP: 19103
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Diskette
21 COMPUTER: IBM Compatible
22 OPERATING SYSTEM: DOS
23 SOFTWARE: FASTSEQ for Windows Version 2.0
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/915.107
26 FILING DATE:
27 CLASSIFICATION: 514
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:
30 FILING DATE:
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Dickinson, Todd Q
33 REGISTRATION NUMBER: 28,354
34 REFERENCE/DOCKET NUMBER: P50549-4
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 215-994-2252
37 TELEFAX: 215-994-2222
38 TELEX:
39 INFORMATION FOR SEQ ID NO: 1:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 1125 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: double
44 TOPOLOGY: linear

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	Query Match	1.4%	Score 40.6:	DB 2	Length 1125:
	Best Local Similarity	46.3%	Pred. No. 0.048:		
	Matches 133:	Conservative	0:	Mismatches 154:	Indels 0:
	Gaps	0:			
Oy	1460 atgagcagcttcgtgcattatgaataatgltgcaggaaattcgtctagcaatgcccta	1519			
b	943 attgagcgacagtcttacctttttaaatgctccaacagcagtaactcttaccacacgacg	884			

[illegible]

50 Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match	4.18;	Score 118.6;	DB 22;	Length 936;
Best Local Similarity	1.38;	Pred. No. 2.8e-23;		
Matches	10;	Conservative 480;	Mismatches 299;	Indels 0;
			Gaps	0;

QY	436	gcgtctataataaagaagcgagacatcgaatccttaacataat	495
Db	789	GCCTTCTATAATAAGAAGCGGAGACATCGAATCCTTAACAT	730
QY	496	aatcagatgctgctgattatgaagaactttctatgccaggagacatagt	555
Db	729	AAATCAGATGCTGCTGATTATGAAGAACTTCTATGCCAGGAGACATAGT	670
QY	556	accgctataacccttgcttgtagcgagcaatcgtctgtttctcttattgacaactc	615
Db	669	AAACGCTATACCCTTGCTTGTAGCGAGCAATCGTCTGTCTCTTATTGACAACCTC	610
QY	616	tgtatcaaacatatacagcaggaanaagctgctcatcgtcgtgaacagacatctc	675
Db	609	TTGTATCAAAACATATACAGCAGGAANAAGCTGCTCATCGTCGTCGTGAACAGACATCTC	550
QY	676	cttgagagtaataactgcgactctctcttcatcaataacgcctgtgtgacgaagacg	735
Db	549	CTTGAGAGTAATAACTGCGACTCTCTCTTCAATAACGCCTGTGTGACGAAGACG	490
QY	736	atctctccctcctatctgctctcacaagaaatcggtgacaatcggtttctcatacaat	795
Db	489	ATCTCTCCCTCCTATCTGCTCTCACAGAAATCGGTGACAATCGGTTTCTCATACAAT	430
QY	796	cgcgtcttaaaaatgtagaacaagcttctcagaagcttctgatggaggaatlaa	855
Db	429	CGCGTCTTAAAAATGTAGAACAGCTTCTCAGAAGCTTCTGATGGAGGAATLAA	370
QY	856	gtactactcgcctagatgltacagccaatcggtgagagatcttctttagtgaacatc	915
Db	369	GTACTACTCGCCTAGATGTLTACAGCCAATCGGTGAGAGATCTCTTTAGTGAACATC	310
QY	916	acaaaataatgatggcagacatttacgcctcctgtagtaccagtatgataatgacct	975
Db	309	ACAAAATAATGATGGCAGACATTTACGCCTCCTGTAGTACCAGTATGATAATGACCT	250
QY	976	acctactttataacaatatcgccaataataaggaggcgctacatctatagacggaac	1035
Db	249	ACCTACTTTATAACAATATCGCCAATAATAAGGAGGCGCTACATCTATAGACGGAAC	190
QY	1036	agcaactccaaaattctgcgcgcgcacatgcatattttaatgaaatatgtgact	1095
Db	189	AGCAACTCCAAAATCTGCGCGCGCACATGCTATTTTAATGAAATATGTGACT	130
QY	1096	aattgaactaatgcaaatggtacagtagtcagtaactcctctagagaagaatgacata	1155
Db	129	AATTGAACTAATGCAAAATGGTACAGTAGTCAGTAACCTCCTAGAGAAGAATGACATA	70
QY	1156	accgtagcaagccctcctgttgaaattcattcattagagcgcggaagtagccaaatlaat	1215
Db	69	AAACGTAGCAAGCCCTCCTGTGAAATTCATTCATCATTAGAGCGCGGAAGTAGCCAAATLAAT	10
QY	1216	tttatgat 1224	
Db	9	TTTTATGAT 1	
RESULT 15			
AAFS8255/c			
ID AAF58255 standard; DNA: 938 BP.			
AAF58255:			
24-APR-2001 (first entry)			
Oligonucleotide D1876.			

```
RESULT 11
AAF58254/C
ID AAF58254 standard; DNA: 936 BP.
XX
AC AAF58254:
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1875.
XX
KM Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Imek RM:
XX
DR WPI: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
CC
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other:

Query Match 4.1%; Score 118.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 2.8e-23;
Matches 10; Conservative 480; Mismatches 299; Indels 0; Gaps 0:

OY 436 gctgttaataaataagaagagcgagccatctgctcacaattctacataatcat 495
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 789 GCWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 730

OY 496 aatcatgattgtgcgattatagaacttctctatgtccgagagagcattagt 555
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 729 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 670

OY 556 accgctaataacttgtgtgtgagcagaatcagctctgttctctcttaagacaatc 615
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 669 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 610

-OY 616 tctattcaaacataacagcagaaaagtgcgctatctatgctgagcagcaattct 675
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 609 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 550

OY 676 tttagagtaataactgcgactctctcttatacaataacgctgtgtgcagagagc 735
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 549 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 490

OY 736 atcttcctccctatctgtctcttaacaggaatcggtgtaacatgcttctataacat 795
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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DB 489 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 430

OY 796 cgtgtcttaaaaaatgagaacagcttctcagaagctctgtagaggaacataaa 855
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DB 429 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 370

OY 856 gtaactactgcctagatgttacagcgaatcgtgtgtagatcttcttaagacaatc 915
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 369 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 310

OY 916 acaaaaattatgtagcagactattacgctccgtgtagtaacctagtggaatgacct 975
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 250

OY 976 acctacttataaacaatcgcacataaataaaggggcgctatctatagacggaacc 1035
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 190

OY 1036 agcaactccaaaattctgtccgaccgcgaatgctattctttaaagaaatattgact 1095
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 130

OY 1096 aatgtaactaatgcaatggtaccagtagcagctaacctcctcagaagaatgcaata 1155
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 70

OY 1156 acagtagcaagctcctcgtgtgaaattctatagagcagagagtagcacaatttcaatc 1215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 10

OY 1216 ttctatgat 1224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 9 WWWWWWWWWWWW 1

RESULT 12
AAF58257/C
ID AAF58257 standard; DNA: 936 BP.
XX
AC AAF58257:
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1954.
XX
KM Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Imek RM:
XX
DR WPI: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
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RESULT      9
AAA28710
ID AAA28710 standard; DNA; 3200 BP.
XX
AC AAA28710;
XX
DT 29-AUG-2000 (first entry)
XX
DE C. pneumoniae CPN100626 gene.
XX
KW Antigen; anti-inflammatory; respiratory; antibacterial; anti-asthmatic;
KW anti-arteriosclerotic; vaccine; ds.
XX
OS Chlamydia pneumoniae.
XX
FH Key Location/Qualifiers
FT CDS 101..3103
FT     /*lag= a
FT
FT MO200024765-A2.
XX
PD 04-MAY-2000.
XX
PE 28-OCT-1999; 99WO-CA00992.
XX
PR 28-OCT-1998; 98US-0106034.
PR 28-OCT-1998; 98US-0106039.
PR 28-OCT-1998; 98US-0106042.
PR 28-OCT-1998; 98US-0106044.
PR 29-OCT-1998; 98US-0106072.
PR 29-OCT-1998; 98US-0106073.
PR 29-OCT-1998; 98US-0106074.
PR 29-OCT-1998; 98US-0106087.
PR 02-NOV-1998; 98US-0106587.
PR 02-NOV-1998; 98US-0106588.
PR 02-NOV-1998; 98US-0107034.
PR 02-NOV-1998; 98US-0107035.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Wang J;
XX
DR WPI: 2000-350688/30.
DR P-PSDB: AAY92832.
XX
PT Chlamydia antigens and the proteins they encode, useful for
PT vaccinating against Chlamydia infections that affect the respiratory
PT tract
XX
PS Claim 2; Fig 21; 226pp; English.
XX
CC The nucleic acids may be used for the recombinant production of the
CC Chlamydia polypeptides (either in vivo or in vitro) according to standard
CC recombinant DNA methodologies. The polypeptides may then be used to
CC vaccinate against Chlamydia infections in mammals. Chlamydia, such as
CC C. pneumoniae, are pathogens responsible for upper respiratory tract
CC infections such as community acquired pneumonia, acute respiratory
CC disease and bronchitis and may be implicated in atherosclerotic changes
CC and asthma. The nucleic acids may also be used as probes for detecting
CC the presence of Chlamydia nucleic acids in samples (and therefore
CC diagnose infections) and the proteins may be used as antigens for the
CC production of antibodies that may be used to detect Chlamydia proteins
CC in samples (e.g. via enzyme linked immunosorbant assay (ELISA)).
XX
SO Sequence 3200 BP; 941 A; 784 C; 598 G; 877 T; 0 other;

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Query Match      4.5%; Score 131.6; DB 21; Length 3200;
Best Local Similarity 45.7%; Pred. No. 1.1e-26;
Matches 759; Conservative 0; Mismatches 859; Indels 42; Gaps 7;

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OY	2258	tatcttctaaaaattactcatgccaaggaagaatgctcttctatgttgaanaagtttct	2317
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RESULT 8			
ID AAA28711 standard; DNA: 3003 BP.			
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AC	XX		
XX	XX		
DT	29-AUG-2000	(first entry)	
XX	XX		
DE	C. pneumoniae CPN100626 open reading frame.		
XX	XX		
KW	Antigen: anti-inflammatory; respiratory; antibacterial; anti-asthmatic;		
KW	anti-arteriosclerotic; vaccine; ds.		
XX	XX		
OS	Chlamydia pneumoniae.		
XX	XX		
PN	WO200024765-A2.		
XX	XX		
PD	04-MAY-2000.		
XX	XX		
PF	28-OCT-1999;	99WO-CA00992.	
XX	XX		
PR	28-OCT-1998;	98US-0106034.	
PR	28-OCT-1998;	98US-0106039.	
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PR	28-OCT-1998;	98US-0106044.	
PR	29-OCT-1998;	98US-0106072.	
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PR	29-OCT-1998;	98US-0106074.	
PR	29-OCT-1998;	98US-0106087.	
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PR	02-NOV-1998;	98US-0106588.	
PR	02-NOV-1998;	98US-0107034.	

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 AAH56262 standard; DNA: 2934 BP.
 ID AAH56262:
 AC AAH56262:
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 XX
 DT 05-SEP-2001 (first entry)
 XX
 XX
 DE Chlamydia trachomatis pmpe gene.
 XX
 KW Chlamydia: vaccine; infection; fusion protein; antigen;
 KW pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;
 KW acute respiratory tract infection; Capli; CT529; OMCB;
 KW polymorphic membrane protein; pmp; thiol specific antioxidant; TSA; ds.
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 OS Chlamydia trachomatis.
 XX
 PN MO200140474-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 04-DEC-2000: 2000MO-US32919.
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 PR 03-DEC-1999: 99US-0454684.
 PR 19-APR-2000: 2000US-0556877.
 PR 20-JUN-2000: 2000US-0598419.
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 PA (CORI-) CORIXA CORP.
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 PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J;
 DR WPI: 2001-374831/39.
 XX
 PT Chlamydia polypeptides and fusion proteins useful for preventing pelvic
 PT inflammatory disease, trachoma, acute respiratory tract infections,
 PT atherosclerosis and heart disease -

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1 (bases 1 to 298283)
Adams,M.D., Celisner,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanalides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galie,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blazer,R.G., Champe,M., Pfeiffer,B.D., Maas,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor,Miklos,G.L., Abail,J.F., Agbayani,A., An,H.J., Andrews-Fannkuch,C., Baldwin,D., Bailey,R.W., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borokova,D., Botchan,M.R., Bouck,J., Brokstein,P., Brotlier,P., Burris,K.C., Busam,D.A., Butler,H., Cadiou,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferrelera,S., Fleischmann,W., Foster,C., Gabrielian,A.E., Garg,N.S., Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Harris,N.L., Harvey,D., Helman,T.J., Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J., Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z., Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Maizel,B., McIntosh,T.C., McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C., Morris,J.J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nusken,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S., Pollard,J., Puri,Y., Reese,M.G., Reinert,K., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I., Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spredling,A.C., Stapleton,M., Strong,R., Sun,E., Svistskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A., Weinstock,G.M., Weissbach,J., Williams,S.M., Woodage,T., Zaverly,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaverly,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,C.J.
The genome sequence of *Drosophila melanogaster*
Science 287 (5461), 2185-2195 (2000)
20196006

TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

2 (bases 1 to 298283)
Adams,M.D., Celisner,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7302138.

Location/Qualifiers

1..298283

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TITLE Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pneumoniae AR39
JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)
MEDLINE 20150255
PUBMED 10684935
AUTHORS 2 (bases 1 to 14482)
Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Uitterback, T.,
Barry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,
Bowman, C., Dodson, R., Gunn, M., Nelson, W., Deboy, R.,
McClarty, G., Salzberg, S.L., Eisen, J., and Fraser, C.M.
Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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ACCESSION
AE002189 AE002161
VERSION
AE002189.2 GI:8163402

KEYWORDS
SOURCE
ORGANISM Chlamydomonada pneumoniae AR39.

REFERENCE
AUTHORS
1 (bases 1 to 10236)
Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Uterback, T.,
Berry, K., Bass, S., Linher, K., Weidman, J., Khouiri, H., Craven, B.,
Bowman, C., Dodson, R., Gwin, M., Nelson, W., Deboy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 10236)
Nucleic Acids Res. 28 (6), 1397-1406 (2000)

10684935

Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Uterback, T.,
Berry, K., Bass, S., Linher, K., Weidman, J., Khouiri, H., Craven, B.,
Bowman, C., Dodson, R., Gwin, M., Nelson, W., Deboy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.

Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
On Jun 1, 2000 this sequence version replaced gi:7189205.

location/Qualifiers
1. 10236

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ORIGIN

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Matches 936; Conservative 0; Mismatches 1116; Indels 61; Gaps 8;
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DB 9074 GGTCCGACACCATTTATTAATCACTGCGACTTCAGAGAGCGCTCTCATCAATCTTTCT 9015

JOURNAL

Submitted (04-JUL-2000) to the DBJ/EMBL/GenBank databases.
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755-8505, Japan (E-mail:ms Shirai@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-2227, Fax:81-836-22-2415)

COMMENT

On Sep 15, 2000 this sequence version replaced g1:6172290
g1:6172292 g1:6172294 g1:6172296 g1:6172326 g1:6172330
g1:6172332 g1:6172334 g1:6172338 g1:6172382 g1:6172384
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g1:6174668 g1:6635174 g1:6635176 g1:6635178 g1:6635180 g1:8547433
g1:8547438 g1:8978640.
AB033782-AB033785, AB033800-AB033815: Submitted (25-Oct-1999)
AB038348-AB038349: Submitted (14-Feb-2000)
AB036079-AB036082: Submitted (18-Dec-2000).

FEATURES

source

1. 300650
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gene

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gene

CDS

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gene

CDS

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gene

CDS

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gene

CDS

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ACCESSION	AE001631	AE001363	
VERSION	AE001631.1	GI:4376750	
KEYWORDS			
SOURCE	Chlamydia pneumoniae CML029.		
ORGANISM	Chlamydia pneumoniae CML029		
REFERENCE	Bacteria: Chlamydiales: Chlamydiales: Chlamydia.		
AUTHORS	1 (bases 1 to 12083)		
TITLE	Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W., Olinger, L., Grimwood, J., Davis, R. W. and Stephens, R. S.		
JOURNAL	Comparative genomes of Chlamydia pneumoniae and C. trachomatis		
MEDLINE	Nat. Genet. 21 (4), 385-389 (1999)		
PUBMED	99206606		
REFERENCE	10192388		
AUTHORS	2 (bases 1 to 12083)		
TITLE	Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L., Grimwood, J., Davis, R. W. and Stephens, R. S.		
JOURNAL	Direct Submission		
FEATURES	Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA		
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